

This Page Is Inserted by IFW Operations  
and is not a part of the Official Record

## **BEST AVAILABLE IMAGES**

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- /• BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

**IMAGES ARE BEST AVAILABLE COPY.**

**As rescanning documents *will not* correct images,  
please do not report the images to the  
Image Problem Mailbox.**



INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification <sup>7</sup> : C12N 15/86, 15/35, 5/10, A61K 48/00	A3	(11) International Publication Number: <b>WO 00/28061</b>
		(43) International Publication Date: 18 May 2000 (18.05.00)
(21) International Application Number: PCT/US99/25694 (22) International Filing Date: 2 November 1999 (02.11.99) (30) Priority Data: 60/107,114      5 November 1998 (05.11.98)      US (71) Applicant ( <i>for all designated States except US</i> ): THE TRUSTEES OF THE UNIVERSITY OF PENNSYLVANIA [US/US]; Suite 300, 3700 Market Street, Philadelphia, PA 19104-3147 (US). (72) Inventors; and (75) Inventors/Applicants ( <i>for US only</i> ): WILSON, James, M. [US/US]; 1350 N. Avignon Drive, Gladwyne, PA 19035 (US). XIAO, Weidong [CN/US]; Apartment P4, 155 Washington Lane, Jenkintown, PA 19046 (US). (74) Agents: KODROFF, Cathy, A. et al.; Howson & Howson, Spring House Corporate Center, P.O. Box 457, Spring House, PA 19477 (US).		(81) Designated States: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).  Published <i>With international search report.</i> (88) Date of publication of the international search report: 3 August 2000 (03.08.00)
(54) Title: ADENO-ASSOCIATED VIRUS SEROTYPE 1 NUCLEIC ACID SEQUENCES, VECTORS AND HOST CELLS CONTAINING SAME		
(57) Abstract  The nucleic acid sequences of adeno-associated virus (AAV) serotype 1 are provided, as are vectors and host cells containing these sequences and functional fragments thereof. Also provided are methods of delivering genes via AAV-I derived vectors.		

Express Mail No. ET033648243US

**FOR THE PURPOSES OF INFORMATION ONLY**

Codes used to identify States party to the PCT on the front pages of pamphlets publishing international applications under the PCT.

AL	Albania	ES	Spain	LS	Lesotho	SI	Slovenia
AM	Armenia	FI	Finland	LT	Lithuania	SK	Slovakia
AT	Austria	FR	France	LU	Luxembourg	SN	Senegal
AU	Australia	GA	Gabon	LV	Larvia	SZ	Swaziland
AZ	Azerbaijan	GB	United Kingdom	MC	Monaco	TD	Chad
BA	Bosnia and Herzegovina	GE	Georgia	MD	Republic of Moldova	TG	Togo
BB	Barbados	GH	Ghana	MG	Madagascar	TJ	Tajikistan
BE	Belgium	GN	Guinea	MK	The former Yugoslav Republic of Macedonia	TM	Turkmenistan
BF	Burkina Faso	GR	Greece	ML	Mali	TR	Turkey
BG	Bulgaria	HU	Hungary	MN	Mongolia	TT	Trinidad and Tobago
BJ	Benin	IE	Ireland	MR	Mauritania	UA	Ukraine
BR	Brazil	IL	Israel	MW	Malawi	UG	Uganda
BY	Belarus	IS	Iceland	MX	Mexico	US	United States of America
CA	Canada	IT	Italy	NE	Niger	UZ	Uzbekistan
CF	Central African Republic	JP	Japan	NL	Netherlands	VN	Viet Nam
CG	Congo	KE	Kenya	NO	Norway	YU	Yugoslavia
CH	Switzerland	KG	Kyrgyzstan	NZ	New Zealand	ZW	Zimbabwe
CI	Côte d'Ivoire	KP	Democratic People's Republic of Korea	PL	Poland		
CM	Cameroon	KR	Republic of Korea	PT	Portugal		
CN	China	KZ	Kazakstan	RO	Romania		
CU	Cuba	LC	Saint Lucia	RU	Russian Federation		
CZ	Czech Republic	LI	Liechtenstein	SD	Sudan		
DE	Germany	LK	Sri Lanka	SE	Sweden		
DK	Denmark	LR	Liberia	SG	Singapore		
EE	Estonia						

## ADENO-ASSOCIATED VIRUS SEROTYPE I NUCLEIC ACID SEQUENCES, VECTORS AND HOST CELLS CONTAINING SAME

This work was supported by the National Institutes of Health, grant no. P30 DK47757-06 and PO1 HD32649-04. The US government may have certain rights in  
5 this invention.

### Field of the Invention

This invention relates generally to viral vector, and more particularly, to recombinant viral vectors useful for gene delivery.

### Background of the Invention

10 Adeno-associated viruses are small, single-stranded DNA viruses which require helper virus to facilitate efficient replication [K.I. Berns, *Parvoviridae: the viruses and their replication*, p. 1007-1041, in F.N. Fields et al., Fundamental virology, 3rd ed., vol. 2, (Lippencott-Raven Publishers, Philadelphia, PA) (1995)]. The 4.7 kb genome of AAV is characterized by two inverted terminal repeats (ITR)  
15 and two open reading frames which encode the Rep proteins and Cap proteins, respectively. The Rep reading frame encodes four proteins of molecular weight 78 kD, 68 kD, 52 kD and 40 kD. These proteins function mainly in regulating AAV replication and integration of the AAV into a host cell's chromosomes. The Cap  
20 reading frame encodes three structural proteins in molecular weight 85 kD (VP 1), 72 kD (VP2) and 61 kD (VP3) [Berns, cited above]. More than 80% of total proteins in AAV virion comprise VP3. The two ITRs are the only cis elements essential for AAV replication, packaging and integration. There are two conformations of AAV ITRs  
25 called "flip" and "flop". These differences in conformation originated from the replication model of adeno-associated virus which use the ITR to initiate and reinitiate the replication [R.O. Snyder et al., J. Virol., 67:6096-6104 (1993); K.I. Berns, Microbiological Reviews, 54:316-329 (1990)].

AAVs have been found in many animal species, including primates, canine, fowl and human [F.A. Murphy et al., "The Classification and Nomenclature of Viruses: Sixth Report of the International Committee on Taxonomy of Viruses",

Archives of Virology, (Springer-Verlag, Vienna) (1995)]. In addition to five known primate AAVs (AAV-1 to AAV-5), AAV-6, another serotype closely related to AAV-2 and AAV-1 has also been isolated [E. A. Rutledge et al., J. Virol., 72:309-319 (1998)]. Among all known AAV serotypes, AAV-2 is perhaps the most well-  
5 characterized serotype, because its infectious clone was the first made [R.J. Samulski et al., Proc. Natl. Acad. Sci. USA, 79:2077-2081 (1982)]. Subsequently, the full sequences for AAV-3A, AAV-3B, AAV-4 and AAV-6 have also been determined [Rutledge, cited above; J.A. Chiorini et al., J. Virol., 71:6823-6833 (1997); S. Muramatsu et al., Virol., 221:208-217 (1996)]. Generally, all AAVs share more than  
10 80% homology in nucleotide sequence.

A number of unique properties make AAV a promising vector for human gene therapy [Muzyczka, Current Topics in Microbiology and Immunology, 158:97-129 (1992)]. Unlike other viral vectors, AAVs have not been shown to be associated with any known human disease and are generally not considered pathogenic. Wild type  
15 AAV is capable of integrating into host chromosomes in a site specific manner [R. M. Kotin et al., Proc. Natl. Acad. Sci. USA, 87:2211-2215 (1990)- R.J. Samulski, EMBO J., 10(12):3941-3950 (1991)]. Recombinant AAV vectors can integrate into tissue cultured cells in chromosome 19 if the rep proteins are supplied in *trans* [C. Balague et al., J. Virol., 71:3299-3306 (1997); R. T. Surosky et al., J. Virol.,  
20 71:7951-7959 (1997)]. The integrated genomes of AAV have been shown to allow long term gene expression in a number of tissues, including, muscle, liver, and brain [K. J. Fisher, Nature Med., 3(3):306-312 (1997); R. O. Snyder et al., Nature Genetics, 16:270-276 (1997); X. Xiao et al., Experimental Neurology, 144:113-124 (1997); Xiao, J. Virol., 70(11):8098-8108 (1996)].

25 AAV-2 has been shown to be present in about 80-90% of the human population. Earlier studies showed that neutralizing antibodies for AAV-2 are prevalent [W. P. Parks et al., J. Virol., 2:716-722 (1970)]. The presence of such antibodies may significantly decrease the usefulness of AAV vectors based on AAV-2 despite its other merits. What are needed in the art are vectors characterized by the

advantages of AAV-2, including those described above, without the disadvantages, including the presence of neutralizing antibodies.

#### Summary of the Invention

In one aspect, the invention provides an isolated AAV-1 nucleic acid molecule  
5 which is selected from among SEQ ID NO: 1, the strand complementary to SEQ ID NO: 1, and cDNA and RNA sequences complementary to SEQ ID NO: 1 and its complementary strand.

In another aspect, the present invention provides AAV ITR sequences, which include the 5' ITR sequences, nt 1 to 143 of SEQ ID NO: 1; the 3' ITR sequences, nt  
10 4576 to 4718 of SEQ ID NO: 1, and fragments thereof.

In yet another aspect, the present invention provides a recombinant vector comprising an AAV-1 ITR and a selected transgene. Preferably, the vector comprises both the 5' and 3' AAV-1 ITRs between which the selected transgene is located.

In still another aspect, the invention provides a recombinant vector comprising  
15 an AAV-1 P5 promoter having the sequence of nt 236 to 299 of SEQ ID NO: 1 or a functional fragment thereof.

In a further aspect, the present invention provides a nucleic acid molecule encoding an AAV-1 rep coding region and an AAV-1 cap coding region.

In still another aspect, the present invention provides a host cell transduced with a  
20 recombinant viral vector of the invention. The invention further provides a host cell stably transduced with an AAV-1 P5 promoter of the invention.

In still a further aspect, the present invention provides a pharmaceutical composition comprising a carrier and a vector of the invention.

In yet another aspect, the present invention provides a method for AAV--  
25 mediated delivery of a transgene to a host involving the step of delivering to a selected host a recombinant viral vector comprising a selected transgene under the control of sequences which direct expression thereof and an adeno-associated virus 1 (AAV-1) virion.

In another aspect, the invention provides a method for in vitro production of a selected gene product using a vector of the invention.

Other aspects and advantages of the invention will be readily apparent to one of skill in the art from the detailed description of the invention.

## 5 Brief Description of the Drawings

Figs. 1A-1C illustrate the alignment of nucleotides of AAV-1 [SEQ ID NO: 1], AAV-2 [SEQ ID NO: 18] and AAV-6 [SEQ ID NO: 19]. The alignment was done with MacVector 6.0. The full sequences of AAV-1 are shown in the top line. Nucleotides in AAV-2 and AAV-6 identical to AAV-1 are symbolized by "." and gaps by "-". Some of the conserved features among AAVs are marked in this figure. Note the 3' ITRs of AAV-1 and AAV-6 are shown in different orientations.

Fig. 2 illustrates the predicted secondary structure of AAV-1 ITR. The nucleotides in AAV-2 and AAV-6 are shown in italic and bold respectively.

Fig. 3A illustrates a hypothesis of how AAV-6 arose from the homologous recombination between AAV-1 and AAV-2. The major elements of AAV-1 are indicated in the graph. A region that is shared between AAV-1, AAV-2 and AAV-6 is shown in box with wavy lines.

Fig. 3B is a detailed illustration of a 71 bp homologous region among AAV-1, AAV-2 and AAV-6. Nucleotides that differ among these serotypes are indicated by arrows.

Fig. 4A is a bar chart illustrating expression levels of human alpha 1 anti-trypsin ( $\alpha$ 1AT) in serum following delivery of hAAT via recombinant AAV-1 and recombinant AAV-2 viruses.

Fig. 4B is a bar chart illustrating expression levels of erythropoietin (epo) in serum following delivery of the epo gene via recombinant AAV-1 and recombinant AAV-2 viruses.

Fig. 5A is a bar chart illustrating expression levels of  $\alpha$ 1AT in liver following delivery of  $\alpha$ 1AT as described in Example 7.

Fig. 5B is a bar chart demonstrating expression levels of epo in liver following delivery of epo as described in Example 7.

Fig. 5C is a bar chart demonstrating neutralizing antibodies (NAB) directed to AAV-1 following delivery of  $\alpha$ 1AT or epo to liver as described in Example 7.

5 Fig. 5D is a bar chart demonstrating neutralizing antibodies (NAB) directed to AAV-2 following delivery of  $\alpha$ 1AT or epo to liver as described in Example 7.

Fig. 6A is a bar chart illustrating expression levels of  $\alpha$ 1AT in muscle following delivery of  $\alpha$ 1AT as described in Example 7.

10 Fig. 6B is a bar chart demonstrating expression levels of epo in muscle following delivery of epo as described in Example 7.

Fig. 6C is a bar chart demonstrating neutralizing antibodies (NAB) directed to AAV-1 following delivery of  $\alpha$ 1AT or epo to muscle as described in Example 7.

Fig. 6D is a bar chart demonstrating neutralizing antibodies (NAB) directed to AAV-2 following delivery of  $\alpha$ 1AT or epo to muscle as described in Example 7.

## 15 Detailed Description of the Invention

The present invention provides novel nucleic acid sequences for an adeno-- associated virus of serotype 1 (AAV-1). Also provided are fragments of these AAV-1 sequences. Among particularly desirable AAV-1 fragments are the inverted terminal repeat sequences (ITRs), rep and cap. Each of these fragments may be readily  
20 utilized, e.g., as a cassette, in a variety of vector systems and host cells. Such fragments may be used alone, in combination with other AAV-1 sequences or fragments, or in combination with elements from other AAV or non-AAV viral sequences. In one particularly desirable embodiment, a cassette may contain the AAV-1 ITRs of the invention flanking a selected transgene. In another desirable  
25 embodiment, a cassette may contain the AAV-1 rep and/or cap proteins, e.g., for use in producing recombinant (rAAV) virus.

Thus, the AAV-1 sequences and fragments thereof are useful in production of rAAV, and are also useful as antisense delivery vectors, gene therapy vectors, or vaccine vectors. The invention further provides nucleic acid molecules, gene delivery



vectors, and host cells which contain the AAV-1 sequences of the invention. Also provided a novel methods of gene delivery using AAV vectors.

As described herein, the vectors of the invention containing the AAV-1 capsid proteins of the invention are particularly well suited for use in applications in which the neutralizing antibodies diminish the effectiveness of other AAV serotype based vectors, as well as other viral vectors. The rAAV vectors of the invention are particularly advantageous in rAAV readministration and repeat gene therapy.

These and other embodiments and advantages of the invention are described in more detail below. As used throughout this specification and the claims, the term “comprising” is inclusive of other components, elements, integers, steps and the like.

#### I. AAV-1 NUCLEIC ACID AND PROTEIN SEQUENCES

The AAV-1 nucleic acid sequences of the invention include the DNA sequences of SEQ ID NO: 1 (Figs. 1A-1C), which consists of 4718 nucleotides. The AAV-1 nucleic acid sequences of the invention further encompass the strand which is complementary to SEQ ID NO: 1, as well as the RNA and cDNA sequences corresponding to SEQ ID NO: 1 and its complementary strand. Also included in the nucleic acid sequences of the invention are natural variants and engineered modifications of SEQ ID NO: 1 and its complementary strand. Such modifications include, for example, labels which are known in the art, methylation, and substitution of one or more of the naturally occurring nucleotides with an analog.

Further included in this invention are nucleic acid sequences which are greater than 85%, preferably at least about 90%, more preferably at least about 95%, and most preferably at least about 98 - 99% identical or homologous to SEQ ID NO:1. The term “percent sequence identity” or “identical” in the context of nucleic acid sequences refers to the residues in the two sequences which are the same when aligned for maximum correspondence. The length of sequence identity comparison may be over the full-length sequence, or a fragment at least about nine nucleotides, usually at least about 20 - 24 nucleotides, at least about 28 - 32 nucleotides, and preferably at least about 36 or more nucleotides. There are a number of different

algorithms known in the art which can be used to measure nucleotide sequence identity. For instance, polynucleotide sequences can be compared using Fasta, a program in GCG Version 6.1. Fasta provides alignments and percent sequence identity of the regions of the best overlap between the query and search sequences  
5 (Pearson, 1990, herein incorporated by reference). For instance, percent sequence identity between nucleic acid sequences can be determined using Fasta with its default parameters (a word size of 6 and the NOPAM factor for the scoring matrix) as provided in GCG Version 6.1, herein incorporated by reference.

The term "substantial homology" or "substantial similarity," when referring to  
10 a nucleic acid or fragment thereof, indicates that, when optimally aligned with appropriate nucleotide insertions or deletions with another nucleic acid (or its complementary strand), there is nucleotide sequence identity in at least about 95 - 99% of the sequence.

Also included within the invention are fragments of SEQ ID NO: 1, its  
15 complementary strand, cDNA and RNA complementary thereto. Suitable fragments are at least 15 nucleotides in length, and encompass functional fragments which are of biological interest. Certain of these fragments may be identified by reference to Figs. 1A-1C. Examples of particularly desirable functional fragments include the AAV-1 inverted terminal repeat (ITR) sequences of the invention. In contrast to the 145 nt  
20 ITRs of AAV-2, AAV-3, and AAV-4, the AAV-1 ITRs have been found to consist of only 143 nucleotides, yet advantageously are characterized by the T-shaped hairpin structure which is believed to be responsible for the ability of the AAV-2 ITRs to direct site-specific integration. In addition, AAV-1 is unique among other AAV serotypes, in that the 5' and 3' ITRs are identical. The full-length 5' ITR sequences of  
25 AAV-1 are provided at nucleotides 1-143 of SEQ ID NO: 1 (Fig. 1A) and the full-length 3' ITR sequences of AAV-1 are provided at nt 4576-4718 of SEQ ID NO: 1 (Fig. 1C). One of skill in the art can readily utilize less than the full-length 5' and/or 3' ITR sequences for various purposes and may construct modified ITRs using conventional techniques, e.g., as described for AAV-2 ITRs in Samulski et al, Cell,  
30 33:135-143 (1983).

Another desirable functional fragment of the AAV-1 genome is the P5 promoter of AAV-1 which has sequences unique among AAV P5 promoters, while maintaining critical regulatory elements and functions. This promoter is located within nt 236 - 299 of SEQ ID NO: 1 (Fig. 1A). Other examples of functional fragments of interest include the sequences at the junction of the rep/cap, e.g., the sequences spanning nt 2306-2223, as well as larger fragments which encompass this junction which may comprise 50 nucleotides on either side of this junction. Still other examples of functional fragments include the sequences encoding the rep proteins. Rep 78 is located in the region of nt 334 - 2306 of SEQ ID NO: 1; Rep 68 is located in the region of nt 334-2272, and contains an intron spanning nt 1924-2220 of SEQ ID NO: 1. Rep 52 is located in the region of nt 1007 - 2304 of SEQ ID NO: 1; rep 40 is located in the region of nt 1007 - 2272, and contains an intron spanning nt 1924-2246 of SEQ ID NO: 1. Also of interest are the sequences encoding the capsid proteins, VP 1 [nt 2223-4431 of SEQ ID NO: 1], VP2 [nt 2634-4432 of SEQ ID NO: 1] and VP3 [nt 2829-4432 of SEQ ID NO: 1]. Other fragments of interest may include the AAV-1 P19 sequences, AAV-1 P40 sequences, the rep binding site, and the terminal resolute site (TRS).

The invention further provides the proteins and fragments thereof which are encoded by the AAV-1 nucleic acids of the invention. Particularly desirable proteins include the rep and cap proteins, which are encoded by the nucleotide sequences identified above. These proteins include rep 78 [SEQ ID NO:5], rep 68 [SEQ ID NO:7], rep 52 [SEQ ID NO:9], rep 40 [SEQ ID NO: 11], vpl [SEQ ID NO: 13], vp2 [SEQ ID NO: 15], and vp3 [SEQ IID NO: 17] and functional fragments thereof while the sequences of the rep and cap proteins have been found to be closely related to those of AAV-6, there are differences in the amino acid sequences (see Table 1 below), as well as differences in the recognition of these proteins by the immune system. However, one of skill in the art may readily select other suitable proteins or protein fragments of biological interest. Suitably, such fragments are at least 8 amino acids in length. However, fragments of other desired lengths may be readily utilized.

Such fragments may be produced recombinantly or by other suitable means, e.g., chemical synthesis.

The sequences, proteins, and fragments of the invention may be produced by any suitable means, including recombinant production, chemical synthesis, or other synthetic means. Such production methods are within the knowledge of those of skill in the art and are not a limitation of the present invention.

## II. VIRAL VECTORS

In another aspect, the present invention provides vectors which utilize the AAV-1 sequences of the invention, including fragments thereof, for delivery of a heterologous gene or other nucleic acid sequences to a target cell. Suitably, these heterologous sequences (i.e., a transgene) encode a protein or gene product which is capable of being expressed in the target cell. Such a transgene may be constructed in the form of a "minigene". Such a "minigene" includes selected heterologous gene sequences and the other regulatory elements necessary to transcribe the gene and express the gene product in a host cell. Thus, the gene sequences are operatively linked to regulatory components in a manner which permit their transcription. Such components include conventional regulatory elements necessary to drive expression of the transgene in a cell containing the viral vector. The minigene may also contain a selected promoter which is linked to the transgene and located, with other regulatory elements, within the selected viral sequences of the recombinant vector.

Selection of the promoter is a routine matter and is not a limitation of this invention. Useful promoters may be constitutive promoters or regulated (inducible) promoters, which will enable control of the timing and amount of the transgene to be expressed. For example, desirable promoters include the cytomegalovirus (CMV) immediate early promoter/enhancer [see, e.g., Boshart et al, Cell, 41:521-530 (1985)], the Rous sarcoma virus LTR promoter/enhancer, and the chicken cytoplasmic  $\beta$ -actin promoter [T. A. Kost et al, Nucl. Acids Res., 11(23):8287 (1983)]. Still other desirable promoters are the albumin promoter and an AAV P5 promoter. Optionally, the selected promoter is used in conjunction with a heterologous enhancer, e.g., the  $\beta$ -

actin promoter may be used in conjunction with the CMV enhancer. Yet other suitable or desirable promoters and enhancers may be selected by one of skill in the art.

The minigene may also desirably contain nucleic acid sequences heterologous to the viral vector sequences including sequences providing signals required for efficient polyadenylation of the transcript (poly-A or pA) and introns with functional splice donor and acceptor sites. A common poly-A sequence which is employed in the exemplary vectors of this invention is that derived from the papovavirus SV-40. The poly-A sequence generally is inserted in the minigene downstream of the transgene sequences and upstream of the viral vector sequences. A common intron sequence is also derived from SV-40, and is referred to as the SV40 T intron sequence. A minigene of the present invention may also contain such an intron, desirably located between the promoter/enhancer sequence and the transgene. Selection of these and other common vector elements are conventional [see, e.g., Sambrook et al, "Molecular Cloning. A Laboratory Manual", 2d edit., Cold Spring Harbor Laboratory, New York (1989) and references cited therein] and many such sequences are available from commercial and industrial sources as well as from Genebank.

The selection of the transgene is not a limitation of the present invention. Suitable transgenes may be readily selected from among desirable reporter genes, therapeutic genes, and optionally, genes encoding immunogenic polypeptides. Examples of suitable reporter genes include  $\beta$ -galactosidase ( $\beta$ -gal), an alkaline phosphatase gene, and green fluorescent protein (GFP). Examples of therapeutic genes include, cytokines, growth factors, hormones, and differentiation factors, among others. The transgene may be readily selected by one of skill in the art. See, e.g., WO 98/09657, which identifies other suitable transgenes.

Suitably, the vectors of the invention contain, at a minimum, cassettes which consist of fragments of the AAV-1 sequences and proteins. In one embodiment, a vector of the invention comprises a selected transgene, which is flanked by a 5' ITR and a 3' ITR, at least one of which is an AAV-1 ITR of the invention. Suitably,

vectors of the invention may contain a AAV-1 P5 promoter of the invention. In yet another embodiment, a plasmid or vector of the invention contains AAV-1 rep sequences. In still another embodiment, a plasmid or vector of the invention contains at least one of the AAV-1 cap proteins of the invention. Most suitably, these AAV-1-derived vectors are assembled into viral vectors, as described herein.

A. AAV Viral Vectors

In one aspect, the present invention provides a recombinant AAV-1 viral vector produced using the AAV-1 capsid proteins of the invention. The packaged rAAV-1 virions of the invention may contain, in addition to a selected minigene, other AAV-1 sequences, or may contain sequences from other AAV serotypes.

Methods of generating rAAV virions are well known and the selection of a suitable method is not a limitation on the present invention. See, e.g., K. Fisher et al, J. Virol., 70:520-532 (1993) and US Patent 5,478,745. In one suitable method, a selected host cell is provided with the AAV sequence encoding a rep protein, the gene encoding the AAV cap protein and with the sequences for packaging and subsequent delivery. Desirably, the method utilizes the sequences encoding the AAV-1 rep and/or cap proteins of the invention.

In one embodiment, the rep/cap genes and the sequences for delivery are supplied by co-transfection of vectors carrying these genes and sequences. In one currently preferred embodiment, a cis (vector) plasmid, a trans plasmid containing the rep and cap genes, and a plasmid containing the adenovirus helper genes are co-transfected into a suitable cell line, e.g., 293. Alternatively, one or more of these functions may be provided in trans via separate vectors, or may be found in a suitably engineered packaging cell line.

An exemplary cis plasmid will contain, in 5' to 3' order, AAV 5' ITR, the selected transgene, and AAV 3' ITR. In one desirable embodiment, at least one of the AAV ITRs is a 143 nt AAV-1 ITR. However, other AAV serotype ITRs may be readily selected. Suitably, the full-length ITRs are utilized. However, one of skill in

the art can readily prepare modified AAV-ITRs using conventional techniques. Similarly, methods for construction of such plasmids is well known to those of skill in the art.

A trans plasmid for use in the production of the rAAV-1 virion particle  
5 may be prepared according to known techniques. In one desired embodiment, this plasmid contains the rep and cap proteins of AAV-1, or functional fragments thereof. Alternatively, the rep sequences may be from another selected AAV serotype.

The cis and trans plasmid may then be co-transfected with a wild-type helper virus (e.g., Ad2, Ad5, or a herpesvirus), or more desirably, a replication -  
10 defective adenovirus, into a selected host cell. Alternatively, the cis and trans plasmid may be co-transfected into a selected host cell together with a transfected plasmid which provides the necessary helper functions. Selection of a suitable host cell is well within the skill of those in the art and include such mammalian cells as 293 cells, HeLa cells, among others.

15 Alternatively, the cis plasmid and, optionally the trans plasmid, may be transfected into a packaging cell line which provides the remaining helper functions necessary for production of a rAAV containing the desired AAV-1 sequences of the invention. An example of a suitable packaging cell line, where an AAV-2 capsid is desired, is B-50, which stably expresses AAV-2 rep and cap genes under the control  
20 of a homologous P5 promoter. This cell line is characterized by integration into the cellular chromosome of multiple copies (at least 5 copies) of P5-rep-cap gene cassettes in a concatomer form. This B-50 cell line was deposited with the American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209, on September 18, 1997 under Accession No. CRL-12401 pursuant to the  
25 provisions of the Budapest Treaty. However, the present invention is not limited as to the selection of the packaging cell line.

Exemplary transducing vectors based on AAV-1 capsid proteins have been tested both *in vivo* and *in vitro*, as described in more detail in Example 4. In these studies, it was demonstrated that recombinant AAV vector with an AAV-1  
30 virion can transduce both mouse liver and muscle. These, and other AAV-1 based

gene therapy vectors which may be generated by one of skill in the art are beneficial for gene delivery to selected host cells and gene therapy patients since the neutralization antibodies of AAV-1 present in much of the human population exhibit different patterns from other AAV serotypes and therefore do not neutralize the AAV-1 virions. One of skill in the art may readily prepare other rAAV viral vectors containing the AAV-1 capsid proteins provided herein using a variety of techniques known to those of skill in the art. One may similarly prepare still other rAAV viral vectors containing AAV-1 sequence and AAV capsids of another serotype.

B. Other Viral Vectors

One of skill in the art will readily understand that the AAV-1 sequences of the invention can be readily adapted for use in these and other viral vector systems for *in vitro*, *ex vivo* or *in vivo* gene delivery. Particularly well suited for use in such viral vector systems are the AAV-1 ITR sequences, the AAV-1 rep, the AAV-1 cap, and the AAV-1 P5 promoter sequences.

For example, in one desirable embodiment, the AAV-1 ITR sequences of the invention may be used in an expression cassette which includes AAV-1 5' ITR, a non-AAV DNA sequences of interest (e.g., a minigene), and 3' ITR and which lacks functional rep/cap. Such a cassette containing an AAV-1 ITR may be located on a plasmid for subsequent transfection into a desired host cell, such as the cis plasmid described above. This expression cassette may further be provided with an AAV capsid of a selected serotype to permit infection of a cell or stably transfected into a desired host cell for packaging of rAAV virions. Such an expression cassette may be readily adapted for use in other viral systems, including adenovirus systems and lentivirus systems. Methods of producing Ad/AAV vectors are well known to those of skill in the art. One desirable method is described in PCT/US95/14018. However, the present invention is not limited to any particular method.

Another aspect of the present invention is the novel AAV-1 P5 promoter sequences which are located in the region spanning nt 236 - 299 of SEQ ID NO: 1. This promoter is useful in a variety of viral vectors for driving expression of a desired transgene.



Similarly, one of skill in the art can readily select other fragments of the AAV-1 genome of the invention for use in a variety of vector systems. Such vector systems may include, e.g., lentiviruses, retroviruses, poxviruses, vaccinia viruses, and adenoviral systems, among others. Selection of these vector systems is not a

5 limitation of the present invention.

C. Host Cells And Packaging Cell Lines

In yet another aspect, the present invention provides host cells which may be transiently transfected with AAV-1 nucleic acid sequences of the invention to permit expression of a desired transgene or production of a rAAV particle. For

10 example, a selected host cell may be transfected with the AAV-1 P5 promoter sequences and/or the AAV-1 5' ITR sequences using conventional techniques.

Providing AAV helper functions to the transfected cell lines of the invention results in packaging of the rAAV as infectious rAAV particles. Such cell lines may be produced in accordance with known techniques [see, e.g., US Patent No. 5,658,785], making

15 use of the AAV-1 sequences of the invention.

Alternatively, host cells of the invention may be stably transfected with a rAAV expression cassette of the invention, and with copies of AAV-1 rep and cap genes. Suitable parental cell lines include mammalian cell lines and it may be desirable to select host cells from among non-simian mammalian cells. Examples of suitable

20 parental cell lines include, without limitation, HeLa [ATCC CCL 2], A549 [ATCC Accession No. CCL 185], KB [CCL 17], Detroit [e.g., Detroit 510, CCL 72] and WI-38 [CCL 75] cells. These cell lines are all available from the American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 USA. Other suitable parent cell lines may be obtained from other sources and may be used to

25 construct stable cell lines containing the P5 and/or AAV rep and cap sequences of the invention.

Recombinant vectors generated as described above are useful for delivery of the DNA of interest to cells.

### III. METHODS OF DELIVERING GENES VIA AAV-1 DERIVED VECTORS

In another aspect, the present invention provides a method for delivery of a transgene to a host which involves transfecting or infecting a selected host cell with a recombinant viral vector generated with the AAV-1 sequences (or functional  
5 fragments thereof) of the invention. Methods for delivery are well known to those of skill in the art and are not a limitation of the present invention.

In one desirable embodiment, the invention provides a method for AAV--mediated delivery of a transgene to a host. This method involves transfecting or infecting a selected host cell with a recombinant viral vector containing a selected  
10 transgene under the control of sequences which direct expression thereof and AAV-1 capsid proteins.

Optionally, a sample from the host may be first assayed for the presence of antibodies to a selected AAV serotype. A variety of assay formats for detecting neutralizing antibodies are well known to those of skill in the art. The selection of  
15 such an assay is not a limitation of the present invention. See, e.g., Fisher et al, Nature Med., 3(3):306-312 (March 1997) and W. C. Manning et al, Human Gene Therapy, 9:477-485 (March 1, 1998). The results of this assay may be used to determine which AAV vector containing capsid proteins of a particular serotype are preferred for delivery, e.g., by the absence of neutralizing antibodies specific for that  
20 capsid serotype.

In one aspect of this method, the delivery of vector with AAV-1 capsid proteins may precede or follow delivery of a gene via a vector with a different serotype AAV capsid protein. Thus, gene delivery via rAAV vectors may be used for repeat gene delivery to a selected host cell. Desirably, subsequently administered  
25 rAAV vectors carry the same transgene as the first rAAV vector, but the subsequently administered vectors contain capsid proteins of serotypes which differ from the first vector. For example, if a first vector has AAV-2 capsid proteins, subsequently administered vectors may have capsid proteins selected from among the other serotypes, including AAV-1, AAV-3A, AAV-3B, AAV-4 and AAV-6.

Thus, a rAAV-1-derived recombinant viral vector of the invention provides an efficient gene transfer vehicle which can deliver a selected transgene to a selected host cell *in vivo* or *ex vivo* even where the organism has neutralizing antibodies to one or more AAV serotypes. These compositions are particularly well suited to gene  
5 delivery for therapeutic purposes. However, the compositions of the invention may also be useful in immunization. Further, the compositions of the invention may also be used for production of a desired gene product *in vitro*.

The above-described recombinant vectors may be delivered to host cells according to published methods. An AAV viral vector bearing the selected transgene  
10 may be administered to a patient, preferably suspended in a biologically compatible solution or pharmaceutically acceptable delivery vehicle. A suitable vehicle includes sterile saline. Other aqueous and non-aqueous isotonic sterile injection solutions and aqueous and non-aqueous sterile suspensions known to be pharmaceutically acceptable carriers and well known to those of skill in the art may be employed for  
15 this purpose.

The viral vectors are administered in sufficient amounts to transfect the cells and to provide sufficient levels of gene transfer and expression to provide a therapeutic benefit without undue adverse effects, or with medically acceptable physiological effects, which can be determined by those skilled in the medical arts.  
20 Conventional and pharmaceutically acceptable routes of administration include, but are not limited to, direct delivery to the liver, oral, intranasal, intravenous, intramuscular, subcutaneous, intradermal, and other parental routes of administration. Routes of administration may be combined, if desired.

Dosages of the viral vector will depend primarily on factors such as the  
25 condition being treated, the age, weight and health of the patient, and may thus vary among patients. For example, a therapeutically effective human dosage of the viral vector is generally in the range of from about 1 ml to about 100 ml of solution containing concentrations of from about  $1 \times 10^9$  to  $1 \times 10^{16}$  genomes virus vector. A preferred human dosage may be about  $1 \times 10^{13}$  to  $1 \times 10^{16}$  AAV genomes. The  
30 dosage will be adjusted to balance the therapeutic benefit against any side effects and

such dosages may vary depending upon the therapeutic application for which the recombinant vector is employed. The levels of expression of the transgene can be monitored to determine the frequency of dosage resulting in viral vectors, preferably AAV vectors containing the minigene. Optionally, dosage regimens similar to those described for therapeutic purposes may be utilized for immunization using the compositions of the invention. For *in vitro* production, a desired protein may be obtained from a desired culture following transfection of host cells with a rAAV containing the gene encoding the desired protein and culturing the cell culture under conditions which permits expression. The expressed protein may then be purified and isolated, as desired. Suitable techniques for transfection, cell culturing, purification, and isolation are known to those of skill in the art.

The following examples illustrate several aspects and embodiments of the invention.

#### Example 1 - Generation of Infectious Clone of AAV-1

The replicated form DNA of AAV-1 was extracted from 293 cells that were infected by AAV-1 and wild type adenovirus type 5.

##### A. Cell Culture and Virus

AAV-free 293 cells and 84-31 cells were provided by the human application laboratory of the University of Pennsylvania. These cells were cultured in Dulbecco's Modified Eagle Medium with 10% fetal bovine serum (Hyclone), penicillin (100 U/ml) and streptomycin at 37°C in a moisturized environment supplied with 5% CO<sub>2</sub>. The 84-31 cell line constitutively expresses adenovirus genes E1a, E1b, E4/ORF6, and has been described previously [K. J. Fisher, *J. Virol.*, 70:520-532 (1996)]. AAV-1 (ATCC VR-645) seed stock was purchased from American Type Culture Collection (ATCC, Manassas, VA). AAV viruses were propagated in 293 cells with wild type Ad5 as a helper virus.

##### B. Recombinant AAV Generation

The recombinant AAV viruses were generated by transfection using an adenovirus free method. Briefly, the cis plasmid (with AAV ITR), trans plasmid (with

AAV rep gene and cap gene) and helper plasmid (pFΔ13, with essential regions from the adenovirus genome) were simultaneously co-transfected into 293 cells in a ratio of 1:1:2 by calcium phosphate precipitation. The pFΔ13 helper plasmid has an 8 kb deletion in the adenovirus E2B region and has deletions in most of the late genes.

- 5 This helper plasmid was generated by deleting the RsrII fragment from pFG140 (Microbix, Canada). Typically, 50 μg of DNA (cis:trans:PFΔ13 at ratios of 1:1:2, respectively) was transfected onto a 15 cm tissue culture dish. The cells were harvested 96 hours post-transfection, sonicated and treated with 0.5% sodium deoxycholate (37°C for 10 min). Cell lysates were then subjected to two rounds of a
- 10 CsCl gradient. Peak fractions containing AAV vector were collected, pooled, and dialyzed against PBS before injecting into animals. To make rAAV virus with AAV-1 virion, the pAV1H or p5E18 (2/1) was used as the *trans* plasmid to provide rep and cap function.

- For the generation of rAAV based on AAV-2, p5E18 was used as the
- 15 *trans* plasmid since it greatly improved the rAAV yield. This plasmid, p5E18(2/2), expresses AAV-2 Rep and Cap and contains a P5 promoter relocated to a position 3' to the Cap gene, thereby minimizing expression of Rep78 and Rep68. The strategy was initially described by Li et al, J. Virol., 71:5236-5243 (1997). P5E18(2/2) was constructed in the following way. The previously described pMMTV-trans vector
- 20 (i.e., the mouse mammary tumor virus promoter substituted for the P5 promoter in an AAV-2-based vector) was digested with *Sma*I and *Cla*I, filled in with the Klenow enzyme, and then recircularized with DNA ligase. The resulting construct was digested with *Xba*I, filled in, and ligated to the blunt-ended BamHI-*Xba*I fragment from pCR-p5, constructed in the following way. The P5 promoter of AAV was
- 25 amplified by PCR and the amplified fragment was subsequently cloned into pCR2.1 (Invitrogen) to yield pCR-P5. The helper plasmid pAV1H was constructed by cloning the *Bfa*I fragment of pAAV-2 into pBluescript II-SK(+) at the *Bco*rV and *Sma*I sites. The 3.0-kb *Xba*I-*Kpn*I fragment from p5E18(2/2), the 2.3-kb *Xba*I-*Kpn*I fragment from pAV1H, and the 1.7-kb *Kpn*I fragment from p5E18(2/2) were incorporated into
- 30 a separate plasmid P5E18(2/1), which contains AAV-2 Rep, AAV-1 Cap, and the

AAV-2 P5 promoter located 3' to the Cap gene. Plasmid p5E18(2/1) produced 10- to 20-fold higher quantities of the vector than pAV1H (i.e.,  $10^{12}$  genomes/50 15-cm<sup>2</sup> plates).

### C. DNA Techniques

5 Hirt DNA extraction was performed as described in the art with minor modification [R.J. Samulski et al., Cell, 33:135-143 (1983)]. More particularly, Hirt solution without SDS was used instead of using original Hirt solution containing SDS. The amount of SDS present in the original Hirt solution was added after the cells had been fully suspended. To construct AAV-1 infectious clone, the Hirt DNA from  
10 AAV-1 infected 293 cells was repaired with Klenow enzyme (New England Biolabs) to ensure the ends were blunt. The treated AAV-1 Hirt DNA was then digested with *Bam*HI and cloned into three vectors, respectively. The internal *Bam*HI was cloned into pBlueScript II-SK+ cut with *Bam*HI to get pAV1-BM. The left and right fragments were cloned into pBlueScript II-SK+ cut with *Bam*HI + *Eco*RV to obtain  
15 pAV1-BL and pAV1-BR, respectively. The AAV sequence in these three plasmids were subsequently assembled into the same vector to get AAV-1 infectious clone pAAV-1. The helper plasmid for recombinant AAV-1 virus generation was constructed by cloning the Bfa I fragment of pAAV-1 into pBlueScript II-SK+ at the *Eco*RV site.

20 Analysis of the Hirt DNA revealed three bands, a dimer at 9.4 kb, a monomer at 4.7 kb and single-stranded DNA at 1.7 kb, which correlated to different replication forms of AAV-1. The monomer band was excised from the gel and then digested with *Bam*HI. This resulted in three fragments of 1.1 kb, 0.8 kb and 2.8 kb. This pattern is in accordance with the description by Bantel-schaal and zur Hausen,  
25 Virol., 134(1):52-63 (1984). The 1.1 kb and 2.8 kb *Bam*HI fragments were cloned into pBlueScript-KS(+) at *Bam*HI and *Eco*RV site. The internal 0.8 kb fragment was cloned into *Bam*HI site of pBlueScript-KS(+).

These three fragments were then subcloned into the same construct to obtain a plasmid (pAAV-1) that contained the full sequence of AAV-1. The pAAV-1  
30 was then tested for its ability to rescue from the plasmid backbone and package

infectious virus. The pAAV-1 was then transfected to 293 cells and supplied with adenovirus type as helper at MOI 10. The virus supernatant was used to reinfect 293 cells.

For Southern blot analysis, Hirt DNA was digested with *DpnI* to  
5 remove bacteria-borne plasmid and probed with internal *BamHI* fragment of AAV-1. The membrane was then washed at high stringency conditions, which included: twice 30 minutes with 2X SSC, 0.1% SDS at 65°C and twice 30 minutes with 0.1X SSC, 0.1% SDS at 65°C. The membrane was then analyzed by both phosphor image and X-ray autoradiography. The results confirmed that pAAV-1 is indeed an infectious  
10 clone of AAV serotype 1.

#### Example 2 - Sequencing Analysis of AAV-1

The entire AAV-1 genome was then determined by automatic sequencing and was found to be 4718 nucleotides in length (Figs. 1A-1C). For sequencing, an ABI 373 automatic sequencer as used to determine the sequences for all plasmids and PCR  
15 fragments related to this study using the FS dye chemistry. All sequences were confirmed by sequencing both plus and minus strands. These sequences were also confirmed by sequencing two independent clones of pAV-BM, pAV-BL and pAV-BR. Since the replicated form of AAV-1 DNA served as the template for sequence determination, these sequences were also confirmed by sequencing a series of PCR  
20 products using original AAV-1 seed stock as a template.

The length of AAV-1 was found to be within the range of the other serotypes: AAV-3 (4726 nucleotides), AAV-4 (4774 nucleotides), AAV-2 (4681 nucleotides), and AAV-6 (4683 nucleotides).

The AAV-1 genome exhibited similarities to other serotypes of adeno-  
25 associated viruses. Overall, it shares more than 80% identity with other known AAV viruses as determined by the computer program Megalign using default settings [DNASTAR, Madison, WI]. The key features in AAV-2 can also be found in AAV-1. First, AAV-1 has the same type of inverted terminal repeat which is capable of forming T-shaped hairpin structures, despite the differences at the nucleotide level

(Figs. 2 and 3). The sequences of right ITRs and left ITRs of AAV-1 are identical. The AAV TR sequence is subdivided into A, A', B, B', C, C', D and D' [Bern, cited above].

These AAV ITR sequences are also virtually the same as those found in AAV-5  
6 right ITR, there being one nucleotide difference in each of A and A' sequence, and the last nucleotide of the D sequence. Second, the AAV-2 rep binding motif [GCTCGCTCGCTCGCTG (SEQ ID NO: 20)] is well conserved. Such motif can also be found in the human chromosome 19 AAV-2 pre-integration region. Finally, non-structural and structural coding regions, and regulatory elements similar to those  
10 of other AAV serotypes also exist in AAV-1 genome.

Although the overall features of AAV terminal repeats are very much conserved, the total length of the AAV terminal repeat exhibits divergence. The terminal repeat of AAV-1 consists of 143 nucleotides while those of AAV-2, AAV-3, and AAV-4 are about 145 or 146 nucleotides. The loop region of AAV-1 ITR most  
15 closely resembles that of AAV-4 in that it also uses TCT instead of the TTT found in AAV-2 and AAV-3. The possibility of sequencing error was eliminated using restriction enzyme digestion, since these three nucleotides are part of the SacI site (gagctc; nt 69-74 of SEQ ID NO: 1). The p5 promoter region of AAV-1 shows more variations in nucleotide sequences with other AAV serotypes. However, it still  
20 maintains the critical regulatory elements. The two copies of YY1 [See, Fig. 1A-1C] sites seemed to be preserved in all known AAV serotypes, which have been shown to be involved in regulating AAV gene expression. In AAV-4, there are 56 additional nucleotides inserted between YY1 and E-box/USF site, while in AAV-1, there are 26 additional nucleotides inserted before the E-box/USF site. The p19 promoter, p40  
25 promoter and polyA can also be identified from the AAV-1 genome by analogy to known AAV serotypes, which are also highly conserved.

Thus, the analysis of AAV terminal repeats of various serotypes showed that the A and A' sequence is very much conserved. One of the reasons may be the Rep binding motif (GCTC)<sub>3</sub>GCTG [SEQ ID NO: 20]. These sequences appear to be  
30 essential for AAV DNA replication and site-specific integration. The same sequence



has also been shown to be preserved in a monkey genome [Samulski, personal communication]. The first 8 nucleotides of the D sequence are also identical in all known AAV serotypes. This is in accordance with the observation of the Srivastava group that only the first 10 nucleotides are essential for AAV packaging [X.S. Wang et al, J. Virol., 71:3077-3082 (1997); X.S. Wang et al, J. Virol., 71:1140-1146 (1997)]. The function of the rest of the D sequences still remain unclear. They may be somehow related to their tissue specificities. The variation of nucleotide in B and C sequence may also suggest that the secondary structure of the ITRs is more critical for its biological function, which has been demonstrated in many previous publications.

### Example 3 - Comparison of AAV-1 Sequences

The nucleotide sequences of AAV-1, obtained as described above, were compared with known AAV sequences, including AAV-2, AAV-4 and AAV-6 using DNA Star Megalign. This comparison revealed a stretch of 71 identical nucleotides shared by AAV-1, AAV-2 and AAV-6. See, Figs. 1A-1C.

This comparison further suggested that AAV-6 is a hybrid formed by homologous recombination of AAV-1 and AAV-2. See, Figs. 3A and 3B. These nucleotides divide the AAV-6 genome into two regions. The 5' half of AAV-6 of 522 nucleotides is identical to that of AAV-2 except in 2 positions. The 3' half of AAV-6 including the majority of the rep gene, complete cap gene and 3' ITR is 98% identical to AAV-1.

Biologically, such recombination may enable AAV-1 to acquire the ability to transmit through the human population. It is also interesting to note that the ITRs of AAV-6 comprise one AAV-1 ITR and one AAV-2 ITR. The replication model of defective parvovirus can maintain this special arrangement. Studies on AAV integration have shown that a majority of AAV integrants carries deletions in at least one of the terminal repeats. These deletions have been shown to be able to be repaired through gene conversion using the other intact terminal repeat as a template. Therefore, it would be very difficult to maintain AAV-6 as a homogenous population

when an integrated copy of AAV-6 is rescued from host cells with helper virus infection. The AAV-6 with two identical AAV-2 ITRs or two identical AAV-1 ITRs should be the dominant variants. The AAV-6 with two AAV-1 ITRs has been observed by Russell's group [Rutledge, cited above (1998)]. So far there is no report  
5 on AAV-6 with two AAV-2 ITRs. Acquisition of AAV-2 P5 promoter by AAV-6 may have explained that AAV-6 have been isolated from human origin while AAV-1 with the same virion has not. The regulation of P5 promoter between different species of AAV may be different *in vivo*. This observation suggests the capsid proteins of AAV were not the only determinants for tissue specificity.

10           Although it is clear that AAV-6 is a hybrid of AAV-1 and AAV-2, AAV-6 has already exhibited divergence from either AAV-1 or AAV-2. There are two nucleotide differences between AAV-6 and AAV-2 in their first 450 nucleotides. There are about 1% differences between AAV-6 and AAV-1 in nucleotide levels from nucleotides 522 to the 3' end. There also exists a quite divergent region (nucleotide  
15 4486-4593) between AAV-6 and AAV-1 (Figs. 1A-1C). This region does not encode any known proteins for AAVs. These differences in nucleotide sequences may suggest that AAV-6 and AAV-1 have gone through some evolution since the recombination took place. Another possible explanation is that there exists another variant of AAV-1 which has yet to be identified. So far, there is no evidence to rule  
20 out either possibility. It is still unknown if other hybrids (AAV-2 to AAV-4, etc.) existed in nature.

The coding region of AAV-1 was deduced by comparison with other known AAV serotypes. Table 1 illustrates the coding region differences between AAV-1 and AAV-6. The amino acid residues are deduced according to AAV-2.

25           With reference to the amino acid position of AAV-1, Table 1 lists the amino acids of AAV-1 which have been changed to the corresponding ones of AAV-6. The amino acids of AAV-1 are shown to the left of the arrow. Reference may be made to SEQ ID NO: 5 of the amino acid sequence of AAV-1 Rep 78 and to SEQ ID NO: 13 for the amino acid sequence of AAV-1 VP1.

Table 1

Coding region variations between AAV-1 and AAV-6

Rep protein (Rep78)		Cap protein (VP1)	
Position(s)	Amino acids	Position(s)	Amino acids
28	S→N	129	L→F
191	Q→H	418	E→D
192	H→D	531	E→K
308	E→D	584	F→L
		598	A→V
		642	N→H

It was surprising to see that the sequence of the AAV-1 coding region is almost identical to that of AAV-6 from position 452 to the end of coding region (99%). The first 508 nucleotides of AAV-6 have been shown to be identical to those of AAV-2 [Rutledge, cited above (1998)]. Since the components of AAV-6 genome seemed to be AAV-2 left ITR – AAV-2 p5 promoter – AAV-1 coding region – AAV-1 right ITR, it was concluded that AAV-6 is a naturally occurred hybrid between AAV-1 and AAV-2.

#### Example 4 - Gene Therapy Vector Based on AAV-1

Recombinant gene transfer vectors based on AAV-1 viruses were constructed by the methods described in Example 1. To produce a hybrid recombinant virus with AAV-1 virion and AAV-2 ITR, the AAV-1 trans plasmid (pAV1H) and the AAV-2 cis-lacZ plasmid (with AAV-2 ITR) were used. The AAV-2 ITR was used in this vector in view of its known ability to direct site-specific integration. Also constructed for use in this experiment was an AAV-1 vector carrying the green fluorescent protein (GFP) marker gene under the control of the immediate early promoter of CMV using pAV1H as the trans plasmid.

A. rAAV-1 Viruses Transfect Host Cells in Vitro

84-31 cells, which are subclones of 293 cells (which express adenovirus E1a, E1b) which stably express E4/ORF5, were infected with rAAV-1 GFP or rAAV-lacZ. High levels of expression of GFP and lacZ was detected in the  
5 cultured 84-31 cells. This suggested that rAAV-1 based vector was very similar to AAV-2 based vectors in ability to infect and expression levels.

B. rAAV-1 Viruses Transfect Cells in Vivo

The performance of AAV-1 based vectors was also tested *in vivo*. The rAAV-1 CMV- $\alpha$ 1AT virus was constructed as follows. The EcoRI fragment of  
10 pAT85 (ATCC) containing human  $\alpha$ 1-antitrypsin ( $\alpha$ 1AT) cDNA fragment was blunted and cloned into PCR (Promega) at a SmaI site to obtain PCR- $\alpha$ 1AT. The CMV promoter was cloned into PCR- $\alpha$ 1AT at the XbaI site. The Alb- $\alpha$ 1AT expression cassette was removed by XhoI and ClaI and cloned into pAV1H at the XbaI site. This vector plasmid was used to generate AAV-1-CMV- $\alpha$ 1AT virus used  
15 in the experiment described below.

For screening human antibodies against AAV, purified AAV virus is lysed with Ripa buffer (10 mM Tris pH 8.2, 1% Triton X-100, 1% SDS, 0.15 M NaCl) and separated in 10% SDS-PAGE gel. The heat inactivated human serum was used at a 1 to 1000 dilution in this assay. The rAAV-1 CMV- $\alpha$ 1AT viruses were  
20 injected into Rag-1 mice through tail vein injection at different dosages. The concentration of human  $\alpha$ 1-antitrypsin in mouse serum was measured using ELISA. The coating antibody is rabbit anti-human human  $\alpha$ 1-antitrypsin (Sigma). The goat-antihuman  $\alpha$ 1-antitrypsin (Sigma) was used as the primary detection antibodies. The sensitivity of this assay is around 0.3 ng/ml to 30 ng/ml. The expression of human  $\alpha$ -  
25 antitrypsin in mouse blood can be detected in a very encouraging level. This result is shown in Table 2.

Table 2

## Human Antitrypsin Expressed in Mouse Liver

Amount of virus injected	Week 2 (ng/ml)	Week 4 (ng/ml)
$2 \times 10^{10}$ genomes	214.2	171.4
$1 \times 10^{10}$ genomes	117.8	109.8
$5 \times 10^{10}$ genomes	64.5	67.8
$2.5 \times 10^{10}$ genomes	30.9	58.4

5  
10  
that AAV-1 based vector would be appropriate for both liver and muscle gene delivery.

Example 5 - Neutralizing Antibodies Against AAV-1

Simple and quantitative assays for neutralizing antibodies (NAB) to AAV-1 and AAV-2 were developed with recombinant vectors. A total of 33 rhesus monkeys  
15 and 77 normal human subjects were screened.

A. *Nonhuman Primates*

Wild-caught juvenile rhesus monkeys were purchased from Covance (Alice, Tex.) and LABS of Virginia (Yemassee, SC) and kept in full quarantine. The monkeys weighed approximately 3 to 4 kg. The nonhuman primates used in the  
20 Institute for Human Gene Therapy research program are purposefully bred in the United States from specific-pathogen-free closed colonies. All vendors are US Department of Agriculture class A dealers. The rhesus macaques are therefore not infected with important simian pathogens, including the tuberculosis agent, major simian lentiviruses (simian immunodeficiency virus and simian retroviruses), and  
25 cercopithecine herpesvirus. The animals are also free of internal and external parasites. The excellent health status of these premium animals minimized the potential for extraneous variables. For this study, serum was obtained from monkeys prior to initiation of any protocol.

NAB titers were analyzed by assessing the ability of serum antibody to inhibit the transduction of reporter virus expressing green fluorescent protein (GFP) (AAV1-GFP or AAV2-GFP) into 84-31 cells. Various dilutions of antibodies preincubated with reporter virus for 1 hour at 37°C were added to 90% confluent cell  
5 cultures. Cells were incubated for 48 hours and the expression of green fluorescent protein was measured by FluoroImaging (Molecular Dynamics). NAB titers were calculated as the highest dilution at which 50% of the cells stained green.

Analysis of NAB in rhesus monkeys showed that 61% of animals tested positive for AAV-1; a minority (24%) has NAB to AAV-2. Over one-third of  
10 animals had antibodies to AAV-1 but not AAV-2 (i.e., were monospecific for AAV-1), whereas no animals were positive for AAV-2 without reacting to AAV-1. These data support the hypothesis that AAV-1 is endemic in rhesus monkeys. The presence of true AAV-2 infections in this group of nonhuman primates is less clear, since cross-neutralizing activity of an AAV-1 response to AAV-2 can not be ruled out. It is  
15 interesting that there is a linear relationship between AAV-2 NAB and AAV-1 NAB in animals that had both.

#### B. *Humans*

For these neutralization antibody assays, human serum samples were incubated at 56°C for 30 min to inactivate complement and then diluted in DMEM.  
20 The virus (rAAV or rAd with either lacZ or GFP) was then mixed with each serum dilution (20X, 400X, 2000X, 4000X, etc.) and incubated for 1 hour at 37°C before applied to 90% confluent cultures of 84-31 cells (for AAV) or Hela cells (for adenovirus) in 96-well plates. After 60 minutes of incubation at culture condition, 100 µl additional media containing 20% FCS was added to make final culture media  
25 containing 10% FCS.

The result is summarized in Table 3.

Table 3

Adenovirus	AAV-1	AAV-2	# of samples	Percentage
-	-	-	41	53.2%
+	-	-	16	20.8%
-	+	-	0	0.0%
-	-	+	2	2.6%
-	+	+	2	2.6%
+	-	+	3	3.9%
+	+	-	0	0.0%
+	+	+	13	16.9%
Total			77	100%

The human neutralizing antibodies against these three viruses seemed to be unrelated since the existence of neutralizing antibodies against AAV are not indications for antibodies against adenovirus. However, AAV requires adenovirus as helper virus, in most of the cases, the neutralizing antibodies against AAV correlated with the existence of neutralizing antibodies to adenovirus. Among the 77 human serum samples screened, 41% of the samples can neutralize the infectivity of recombinant adenovirus based on Ad5. 15/77 (19%) of serum samples can neutralize the transduction of rAAV-1 while 20/77 (20%) of the samples inhibit rAAV-2 transduction at 1 to 80 dilutions or higher. All serum samples positive in neutralizing antibodies for AAV-1 in are also positive for AAV-2. However, there are five (6%) rAAV-2 positive samples that failed to neutralize rAAV-1. In samples that are positive for neutralizing antibodies, the titer of antibodies also varied in the positive ones. The results from screening human sera for antibodies against AAVs supported the conclusion that AAV-1 presents the same epitome as that of AAV-2 to interact

with cellular receptors since AAV-1 neutralizing human serums can also decrease the infectivity of AAV-2. However, the profile of neutralizing antibodies for these AAVs is not identical, there are additional specific receptors for each AAV serotype.

Example 6 - Recombinant AAV Viruses Exhibit Tissue Tropism

5           The recombinant AAV-1 vectors of the invention and the recombinant AAV-2 vectors [containing the gene encoding human  $\alpha$ 1-antitrypsin ( $\alpha$ 1AT) or murine erythropoietin (Epo) from a cytomegalovirus-enhanced  $\beta$ -actin promoter (CB)] were evaluated in a direct comparison to equivalent copies of AAV-2 vectors containing the same vector genes.

10           Recombinant viruses with AAV-1 capsids were constructed using the techniques in Example 1. To make rAAV with AAV-1 virions, pAV1H or p5E18 (2/1) was used as the *trans* plasmid to provide Rep and Cap functions. For the generation of the rAAV based on AAV-2, p5E18(2/2) was used as the *trans* plasmid, since it greatly improved the rAAV yield. [Early experiments indicated similar *in vivo* performances of AAV-1 vectors produced with pAV1H and p5E19 (2/1). All subsequent studies used AAV-1 vectors derived from p5E18(2/1) because of the increased yield.]

20           Equivalent stocks of the AAV-1 and AAV-2 vectors were injected intramuscularly ( $5 \times 10^{10}$  genomes) or liver via the portal circulation ( $1 \times 10^{11}$  genomes) into immunodeficient mice, and the animals (four groups) were analyzed on day 30 for expression of transgene. See, Figs. 4A and 4B.

25           AAV-2 vectors consistently produced 10- to 50-fold more serum erythropoietin or  $\alpha$ 1-antitrypsin when injected into liver compared to muscle. (However, the AAV-1-delivered genes did achieve acceptable expression levels in the liver.) This result was very different from that for AAV-1 vectors, with which muscle expression was equivalent to or greater than liver expression. In fact, AAV-1 outperformed AAV-2 in muscle when equivalent titers based on genomes were administered.



Example 7 - Gene Delivery via rAAV-1

C57BL/6 mice (6- to 8-week old males, Jackson Laboratories) were analyzed for AAV mediated gene transfer to liver following intrasplenic injection of vector (i.e., targeted to liver). A total of  $10^{11}$  genome equivalents of rAAV-1 or rAAV-2 vector  
5 were injected into the circulation in 100  $\mu$ l buffered saline. The first vector contained either an AAV-1 capsid or an AAV-2 capsid and expressed  $\alpha$ 1AT under the control of the chicken  $\beta$ -actin (CB) promoter. Day 28 sera were analyzed for antibodies against AAV-1 or AAV-2 and serum  $\alpha$ 1AT levels were checked. Animals were then injected  
10 with an AAV-1 or AAV-2 construct expressing erythropoietin (Epo, also under the control of the CB promoter). One month later sera was analyzed for serum levels of Epo. The following groups were analyzed (Figs. 5A-5D).

In Group 1, vector 1 was AAV-2 expressing  $\alpha$ 1AT and vector 2 was AAV-2 expressing Epo. Animals generated antibodies against AAV-2 following the first vector administration which prevented the readministration of the AAV-2 based  
15 vector. There was no evidence for cross-neutralizing the antibody to AAV-1.

In Group 2, vector 1 was AAV-1 expressing  $\alpha$ 1AT while vector 2 was AAV-1 expressing Epo. The first vector administration did result in significant  $\alpha$ 1AT expression at one month associated with antibodies to neutralizing antibodies to AAV-1. The animals were not successfully readministered with the AAV-1 Epo  
20 expressing construct.

In Group 3, the effectiveness of an AAV-2 vector expressing Epo injected into a naive animal was measured. The animals were injected with PBS and injected with AAV-2 Epo vector at day 28 and analyzed for Epo expression one month later. The neutralizing antibodies were evaluated at day 28 so we did not expect to see anything  
25 since they received PBS with the first vector injection. This shows that in naive animals AAV-2 is very efficient at transferring the Epo gene as demonstrated by high level of serum Epo one month later.

Group 4 was an experiment similar to Group 3 in which the animals originally received PBS for vector 1 and then the AAV-1 expressing Epo construct 28 days  
30 later. At the time of vector injection, there obviously were no antibodies to either

AAV-1 or AAV-2. The AAV-1 based vector was capable of generating significant expression of Epo when measured one month later.

Group 5 is a cross-over experiment where the initial vector is AAV-2 expressing  $\alpha$ 1AT followed by the AAV-1 construct expressing Epo. The animals, as expected, were efficiently infected with the AAV-2 vector expressing  $\alpha$ 1AT as shown by high levels of the protein in blood at 28 days. This was associated with significant neutralizing antibodies to AAV-2. Importantly, the animals were successfully administered AAV-1 following the AAV-2 vector as shown by the presence of Epo in serum 28 days following the second vector administration. At the time of this vector administration, there was high level AAV-2 neutralizing antibodies and very low cross-reaction to AAV-1. The level of Epo was slightly diminished possibly due to a small amount of cross-reactivity. Group 6 was the opposite cross-over experiment in which the initial vector was AAV-1 based, whereas the second experiment was AAV-2 based. The AAV-1 vector did lead to significant gene expression of  $\alpha$ 1AT, which also resulted in high level AAV-1 neutralizing antibody. The animals were very efficiently administered AAV-2 following the initial AAV-1 vector as evidenced by high level Epo.

A substantially identical experiment was performed in muscle in which  $5 \times 10^{10}$  genomes were injected into the tibialis anterior of C57BL/6 mice as a model for muscle directed gene therapy. The results are illustrated in Figs. 6A-6D and are essentially the same as for liver.

In summary, this experiment demonstrates the utility of using an AAV-1 vector in patients who have pre-existing antibodies to AAV-2 or who had initially received an AAV-2 vector and need readministration.

#### 25 Example 8 - Construction of Recombinant Viruses Containing AAV-1 ITRs

This example illustrates the construction of recombinant AAV vectors which contain AAV-1 ITRs of the invention.

An AAV-1 cis plasmid is constructed as follows. A 160 bp Xho-NruI AAV-1 fragment containing the AAV-1 5' ITR is obtained from pAV1-BL. pAV1-BL was

generated as described in Example 1. The Xho-NruI fragment is then cloned into a second pAV1-BL plasmid at an XbaI site to provide the plasmid with two AAV-1 ITRs. The desired transgene is then cloned into the modified pAV-1BL at the NruI and BamHI site, which is located between the AAV-1 ITR sequences. The resulting  
5 AAV-1 cis plasmid contains AAV-1 ITRs flanking the transgene and lacks functional AAV-1 rep and cap.

Recombinant AAV is produced by simultaneously transfecting three plasmids into 293 cells. These include the AAV-1 cis plasmid described above; a trans plasmid which provides AAV rep/cap functions and lacks AAV ITRs; and a plasmid providing  
10 adenovirus helper functions. The rep and/or cap functions may be provided in trans by AAV-1 or another AAV serotype, depending on the immunity profile of the intended recipient. Alternatively, the rep or cap functions may be provided in cis by AAV-1 or another serotype, again depending on the patient's immunity profile.

In a typical cotransfection, 50 µg of DNA (cis:trans:helper at ratios of 1:1:2,  
15 respectively) is transfected onto a 15 cm tissue culture dish. Cells are harvested 96 hours post transfection, sonicated and treated with 0.5% sodium deoxycholate (37° for 10 min). Cell lysates are then subjected to 2-3 rounds of ultracentrifugation in a cesium gradient. Peak fractions containing rAAV are collected, pooled and dialyzed against PBS. A typical yield is  $1 \times 10^{13}$  genomes/ $10^9$  cells.

20 Using this method, one recombinant virus construct is prepared which contains the AAV-1 ITRs flanking the transgene, with an AAV-1 capsid. Another recombinant virus construct is prepared with contains the AAV-1 ITRs flanking the transgene, with an AAV-2 capsid.

All publications cited in this specification are incorporated herein by reference.  
25 While the invention has been described with reference to a particularly preferred embodiments, it will be appreciated that modifications can be made without departing from the spirit of the invention. Such modifications are intended to fall within the scope of the claims.

What is claimed is:

1. An isolated AAV-1 nucleic acid molecule comprising a sequence selected from the group consisting of:
  - (a) SEQ ID NO: 1;
  - (b) a DNA sequence complementary to SEQ ID NO: 1;
  - (c) cDNA complementary to (a) or (b); and
  - (d) RNA complementary to any of (a) to (c).
2. A nucleic acid molecule comprising an AAV-1 inverted terminal repeat (ITR) sequence selected from the group consisting of:
  - (a) nt 1 to 143 of SEQ ID NO: 1;
  - (b) nt 4576 to 4718 of SEQ ID NO: 1;
  - (c) a nucleic acid sequence complementary to (a) or (b); and
  - (d) a functional fragment of (a), (b), or (c).
3. A recombinant vector comprising a 5' AAV-1 inverted terminal repeat (ITR) and a selected transgene, wherein said ITR has the sequence selected from the group consisting of:
  - (a) nt 1 to 143 of SEQ ID NO: 1;
  - (b) a nucleic acid sequence complementary to (a); and
  - (c) a functional fragment of (a) or (b).
4. The recombinant vector according to claim 3, wherein said vector further comprises a 3' AAV-1 ITR.

5. A recombinant vector comprising a 3' AAV-1 inverted terminal repeat (ITR) and a selected transgene, wherein said ITR has the sequence selected from the group consisting of:

- (a) nt 4576 to 4718 of SEQ ID NO: 1;
- (b) a nucleic acid sequence complementary to (a); and
- (c) a functional fragment of (a) or (b).

6. The recombinant vector according to claim 5, wherein said vector further comprises a 5' AAV-1 ITR.

7. The recombinant vector according to any of claims 3-6, wherein said vector further comprises AAV-1 capsid proteins having the sequence of SEQ ID NO: 13, 15 or 17 or functional fragments thereof.

8. The recombinant vector according to any of claims 3-6, wherein said vector further comprises adenovirus sequences.

9. A recombinant vector comprising an AAV-1 P5 promoter having the sequence of nt 236 to 299 of SEQ ID NO: 1 or a functional fragment thereof.

10. A nucleic acid molecule encoding AAV-1 helper functions, said molecule comprising an AAV rep coding region and an AAV cap coding region, wherein said cap coding region comprises at least one member is selected from the group consisting of:

- (a) vp1, nt 2223 to 4431 of SEQ ID NO: 1;
- (b) vp2, nt 2634 to 4432 of SEQ ID NO: 1; and
- (c) vp3, nt 2829 to 4432 of SEQ ID NO: 1.

11. A nucleic acid molecule encoding AAV-1 helper functions, said molecule comprising an AAV rep coding region and an AAV cap coding region, wherein said rep coding region comprises an AAV-1 rep coding region comprising at least one member selected from the group consisting of:

- (a) rep 78, nt 335 to 2304 of SEQ ID NO: 1;
- (b) rep 68, nt 335 to 2272 of SEQ ID NO: 1 or the cDNA corresponding thereto;
- (c) rep 52, nt 1007 to 2304 of SEQ ID NO: 1; and
- (d) rep 40, nt 1007 to 2272 of SEQ ID NO: 1 or the cDNA corresponding thereto.

12. A host cell transduced with a recombinant viral vector according to any of claims 3-6.

13. A host cell transduced with a nucleic acid molecule according to any of claims 1, 2, 10 or 11.

14. A host cell stably transduced with an AAV-1 P5 promoter having the sequence of nt 236 to 299 of SEQ ID NO: 1.

15. A pharmaceutical composition comprising a carrier and a virus comprising the vector according to any of claims 3-6.

16. A pharmaceutical composition comprising a carrier and a virus comprising the vector according to claim 7.

17. A pharmaceutical composition comprising a carrier and a virus comprising the vector according to claim 8.

18. A method for AAV-mediated delivery of a transgene comprising the step of delivering to a host cell an AAV virion which comprises:

- (a) a capsid comprising at least one capsid protein encoded by an AAV-1 cap gene; and
- (b) a DNA molecule comprising a transgene under the control of regulatory sequences directing its expression.

19. A method for AAV-mediated delivery of a transgene to a host comprising the steps of:

- (a) assaying a sample from the host to determine the presence of neutralizing antibodies specific against any serotype of AAV; and
- (b) delivering to the host an AAV virion which comprises:
  - (i) a capsid comprising at least one capsid protein encoded by a cap gene of an AAV serotype against which the host has no antibodies as determined in step (a); and
  - (ii) a DNA molecule comprising a transgene under the control of regulatory sequences directing its expression.

20. The method according to claim 19, comprising the additional step of repeating steps (a) and (b).

21. Use of an AAV virion which comprises a capsid comprising (a) at least one capsid protein encoded by a cap gene of an AAV serotype against which the host has antibodies, and (b) a DNA molecule comprising a transgene operably linked to regulatory sequences directing its expression,

in the preparation of a medicament for delivery of a transgene to a host, wherein said host has no preexisting neutralizing antibodies against the AAV serotype of said cap gene.

22. A method for delivery of a transgene comprising the step of delivering to a host cell a recombinant virus comprising a recombinant vector according to any of claims 3-8.

23. A method for producing a selected gene product comprising the steps of transfecting a mammalian cell with the molecule according to claim 1 or a functional fragment thereof and culturing said cell under conditions suitable to express said gene product.



1/13

FIG 1A

AAV-1	ttgcccactccctctctgcgcgctcgctcgctcggtggggcctgcggaacaaaggtccgc	60
AAV-2	...g.....ac..a....g.gc.....gc.	60
AAV-6	...g.....ac..a....g.gc.....gc.	60
Rep binding site		
AAV-1	agacggcagagctctgctctgccggccacccagagcgagcgagcgcgagagagggagtg	120
AAV-2	c....c.c.g...t...c.g.g....t..gt.....	120
AAV-6	c....c.c.g...t...c.g.g....t..gt.....	120
TRS		
AAV-1	ggcaactccatcactaggggtaaTCGCGAAGCGCCTCCCACGCTGCCGCGTCAGCGCTGA	180
AAV-2	.c.....--..ct.G..G.-----TG.A...G----...	163
AAV-6	.c.....--..ct.G..G.-----TG.A...G----...	163
E box/USF		
AAV-1	CGTAAATTACGTCATAGGG---GAGTGGTCCTGTATTAGCTGTCACGTGAGTGCTTTTGC	237
AAV-2	...G.....TTA.G.A.....AG.....-.....	222
AAV-6	...G.....TTA.G.A.....AG.....-.....	222
YY1		
P5/TATA		
AAV-1	GACATTTTGCGACACCACGTGGCCATTTAGGGTATATATGGCCGAGTGAGCGAGCAGGAT	297
AAV-2	.....T....T..CGCT.....T..A.C.....AC.....G.	282
AAV-6	.....T....T..CGCT.....T..A.C.....AC.....G.	282
YY1/p5 RNA		
Rep 78/68		
AAV-1	CTCCATTTTGAC-CGCGAAATTTGAACGAGCAGCAGCCATGCCGGGCTTCTACGAGATCG	356
AAV-2	.....AG..G..GG.....C.....C.....G..T.....T.	342
AAV-6	.....AG..G..GG.....C.....-.....G..T.....T.	341
AAV-1	TGATCAAGGTGCCGAGCGACCTGGACGAGCACCTGCCGGGCATTTCTGACTCGTTTGTGA	416
AAV-2	....T.....C..C.....T....G...T....C.....AGC.....	402
AAV-6	....T.....C..C.....T.....T....C.....AGC.....	401
AAV-1	GCTGGGTGGCCGAGAAGGAATGGGAGCTGCCCCCGGATTCTGACATGGATCTGAATCTGA	476
AAV-2	A.....T....G..A.....	462
AAV-6	A.....T....G..A.....	461
AAV-1	TTGAGCAGGCACCCCTGACCGTGGCCGAGAAGCTGCAGCGCGACTTCCTGGTCCAATGGC	536
AAV-2	.....T...ACGG.....	522
AAV-6	.....G.....	521
AAV-1	GCCGCGTGAGTAAGGCCCGGAGGCCCTCTTCTTTGTTTCAGTTCGAGAAGGGCGAGTCCT	596
AAV-2	....T.....T.....G..A..T.....A...AG..	582
AAV-6	.....	581
AAV-1	ACTTCCACCTCCATATTCTGGTGGAGACCACGGGGGTCAAATCCATGGTGCTGGGCGCT	656
AAV-2	.....A.G..CG.G..C.....A....C.....G.....TT....A..T.	642
AAV-6	.....	641
AAV-1	TCCTGAGTCAGATTAGGGACAAGCTGGTGCAGACCATCTACCGCGGGATCGAGCCGACCC	716
AAV-2	.....C.C..A..A...A.T....GA..T.....TT	702
AAV-6	.....	701
AAV-1	TGCCCAACTGGTTCGCGGTGACCAAGACGCGTAATGGCGCCGAGGGGGGAACAAGGTGG	776
AAV-2	....A.....C..A....CA.A.....C.....	762
AAV-6	.....	761

2/13

FIG 1B

AAV-1	TGGACGAGTGCTACATCCCCAACTACCTCCTGCCCAAGACTCAGCCCCGAGCTGCAGTGGG	836
AAV-2	....T.....T...T.G..C.....A..C.....T.....C.....	822
AAV-6	.....	821
P19/TATA		
AAV-1	CGTGGACTAACATGGAGGAGTATATAAGCGCCTGTTTGAACCTGGCCGAGCGCAAACGGC	896
AAV-2	.....T.....AC.....T.....C.....G..T..CA.G.....T.....T	882
AAV-6	.....C.....GG.....A.....G.....A..C..GG.C.....	881
P19 RNA		
AAV-1	TCGTGGCGCAGCACCTGACCCACGTCAGCCAGACCCAGGAGCAGAACAAGGAGAATCTGA	956
AAV-2	.G.....T.....G.....GTCG.....G.....A.....A..	942
AAV-6	.....CG.....	941
Rep 52/40		
AAV-1	ACCCCAATTCTGACGCGCCTGTCATCCGGTCAAAAACCTCCGCGCGCTACATGGAGCTGG	1016
AAV-2	.T.....T.....G..G...A.A.....T..A..CA.G.....	1002
AAV-6	.....A.....	1001
AAV-1	TCGGGTGGCTGGTGGACCGGGGCATCACCTCCGAGAAGCAGTGGATCCAGGAGGACCAGG	1076
AAV-2	.....C.....AA...G..T.....G.....	1062
AAV-6	.....	1061
AAV-1	CCTCGTACATCTCCTTCAACGCGCTTCCAACCTCGCGGTCCCAGATCAAGGCCGCTCTGG	1136
AAV-2	....A.....T..G..C.....A.....T..CT...	1122
AAV-6	.....	1121
AAV-1	ACAATGCCGGCAAGATCATGGCGCTGACCAAATCCGCGCCCGACTACCTGGTAGGCCCCG	1196
AAV-2	.....G..A.....T...AGC.....T...A....C.....G....AGC	1182
AAV-6	.....	1181
AAV-1	CTCCGCCCCGCGGACATTAAAACCAACCGCATCTACCGCATCCTGGAGCTGAACGGCTACG	1256
AAV-2	AG..CGTG.A.....TCC.G...T..G..T..TAAA..TT....A..A.....G....	1242
AAV-6	.....C.....T.....	1241
AAV-1	AACCTGCCTACGCCGGCTCCGTCTTTCTCGGCTGGGCCCAGAAAAGGTTTCGGGAAGCGCA	1316
AAV-2	.T..CCAA..T..G..CT.....G..A.....AC.....A.....C...A.G.	1302
AAV-6	.C.....A..A....	1301
AAV-1	ACACCATCTGGCTGTTTGGGCGCGCCACCACGGGCAAGACCAACATCGCGGAAGCCATCG	1376
AAV-2	.....T..A..T..C..G.....G.....A.	1362
AAV-6	.....	1361
AAV-1	CCCACGCCGTGCCCTTCTACGGCTGCGTCAACTGGACCAATGAGAACTTCCCTTCAATG	1436
AAV-2	....A.T.....G.....A.....C.	1422
AAV-6	.....C.	1421
AAV-1	ATTGCGTCGACAAGATGGTGATCTGGTGGGAGGAGGGCAAGATGACGGCCAAGGTCGTGG	1496
AAV-2	.C..T.....G.....C.....	1482
AAV-6	.....	1481
AAV-1	AGTCCGCCAAGGCCATTCTCGGCGGCAGCAAGGTGCGCGTGGACCAAAAAGTGCAAGTCGT	1556
AAV-2	....G.....A.....A..A.....G..A.....C.	1542
AAV-6	.....	1541
AAV-1	CCGCCCAGATCGACCCACCCCGTGATCGTCACCTCCAACACCAACATGTGCGCCGTGA	1616
AAV-2	.G.....A.....G..T.....	1602
AAV-6	.....	1601

3/13

FIG 1C

AAV-1	TTGACGGGAACAGCACCACCTTCGAGCACCAGCAGCCGTTGCAGGACCGGATGTTCAAAT	1676
AAV-2	.....TCA..G.....A.....A.....	1662
AAV-6	.....	1661
AAV-1	TTGAACTCACCCGCCGTCTGGAGCATGACTTTGGCAAGGTGACAAAGCAGGAAGTCAAAG	1740
AAV-2	.....T.....G.....C..C.....	1722
AAV-6	.....	1721
AAV-1	AGTTCTTCCGCTGGGCGCAGGATCACGTGACCGAGGTGGCGCATGAGTTCTACGTCAGAA	1796
AAV-2	.C..T.....G.....AA.....GTT.....A.....A.....A..	1782
AAV-6	.....	1781
P40/TATA		
AAV-1	AGGGTGGAGCCAACAAAAGACCCGCCCCCGATGACGCGGATAAAAGCGAGCCCCAAGCGGG	1856
AAV-2	.....G.....AG.....A...T...T.....A....	1842
AAV-6	.....G.....	1841
P40 RNA		
AAV-1	CCTGCCCCTCAGTCGCGGATCCATCGACGTCAGACGCGGAAGGAGCTCCGGTGGACTTTG	1916
AAV-2	TGC..GAG.....T...C.G.....---..T..A.CA...AC.	1899
AAV-6	.....	1901
▼		
AAV-1	CCGACAGGTACCAAAACAAATGTTCTCGTCACGCGGGCATGCTTCAGATGCTGTTTCCCT	1976
AAV-2	.A.....T.....AA..T.....	1959
AAV-6	.....	1961
AAV-1	GCAAGACATGCGAGAGAATGAATCAGAATTTCAACATTTGCTTCACGCACGGGACGAGAG	2036
AAV-2	...GACA.....CA..T..C.....T....ACA..A..	2019
AAV-6	....A.....C....	2021
AAV-1	ACTGTTTCAAGTGCTTCCCCGGCGTGTCAGAATCTCAACCGGTC---GTCAGAAAGAGGA	2093
AAV-2	.....T.....T...---.....C..TTCT...GTC..A.A.G	2076
AAV-6	.....A..T.....---.....	2078
AAV-1	CGTATCGGAAACTCTGTGCCATTCATCATCTGCTGGGGCGGGCTCCCGAGATTGCTTGCT	2153
AAV-2	.....A.....G..CTA.....A.CA....AAA..TG..A...---C.....A	2133
AAV-6	.....	2138
Rep 78 stop		
AAV-1	CGGCCTGCGATCTGGTCAACGTGGACCTGGATGACTGTGTTTCTGAGCAATAAATGACTT	2213
AAV-2	.T.....T.....TT.....CA.C.T...A.....T..	2193
AAV-6	.....T.....	2193
▽ VP1		
AAV-1	AAACCAGGTATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAG	2273
AAV-2	...T.....CT.....A	2253
AAV-6	.....AC.....G	2258
AAV-1	GGCATTTCGCGAGTGGTGGGACTTGAAACCTGGAGCCCCGAAGCCCAAGCCAACCAGCAA	2333
AAV-2	..A..AA.AC.....A.GC.C.....CC.A..ACCA..A..GC..GCAG...GG	2313
AAV-6	.....A.....	2318
AAV-1	AAGCAGGACGACGGCCGGGGTCTGGTGCTTCTGGCTACAAGTACCTCGGACCCTTCAAC	2393
AAV-2	C.TA.....A..A.....T.....G.....	2373
AAV-6	.....G..C.....G.....C.....	2378

4/13

FIG 1D

AAV-1	GGACTCGACAAGGGGGAGCCCGTCAACGCGCGGACGCAGCGGCCCTCGAGCACGACAAG	2453
AAV-2	.....A.....G.....A...A.....C.....A	2433
AAV-6	.....T.....	2438
AAV-1	GCCTACGACCAGCAGCTCAAAGCGGGTGACAATCCGTACCTGCGGTATAACCACGCCGAC	2513
AAV-2	.....G.....G.CAGC..A.....C.....CAA...C.....	2493
AAV-6	.....A.AGCG..T....T.....GCG...T.....	2498
AAV-1	GCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGGCAACCTCGGGCGAGCA	2573
AAV-2	..G.....C..TA.....A.....	2553
AAV-6	..C.....T..GC.....G.....	2558
AAV-1	GTCTTCCAGGCCAAGAAGCGGGTTCTCGAACCTCTCGGTCTGGTTGAGGAAGGCGCTAAG	2633
AAV-2	.....G..A..A.....T.....G..C.....CCT.T....	2613
AAV-6	.....A.....T.T.....T.....	2618
<u>VP2</u>		
AAV-1	ACGGCTCCTGGAAAGAAACGTCCGGTAGAGCAGTCGCCACAAGAGCCAGACTCCTCCTCG	2693
AAV-2	.....G.....A..GA.G.....C..T..TGTG.....	2673
AAV-6	.....T.....G..AC.T.....G..G..ACAA.....	2678
AAV-1	GGCATCGGCAAGACAGGCCAGCAGCCCGCTAAAAAGAGACTCAATTTTGGTCAGACTGGC	2753
AAV-2	..A.C...A...G.G.....T..A.G...A...T.G.....A	2733
AAV-6	.....T.....	2738
AAV-1	GACTCAGAGTCAGTCCCCGATCCACAACCTCTCGGAGAACCTCCAGCAACCCCCGCTGCT	2813
AAV-2	...G....C.....A..T..C..C..G.....C.G..A.....G....T...G.	2793
AAV-6	...T....G....C..C..C..A..A.....G.A..T.....A....G.....	2798
<u>VP3</u>		
AAV-1	GTGGGACCTACTACAATGGCTTCAGGCGGTGGCGCACCAATGGCAGACAATAACGAAGGC	2873
AAV-2	C.....A...A..G.....A.....A.....G....	2853
AAV-6	.....	2858
AAV-1	GCCGACGGAGTGGGTAATGCCTCAGGAATTGGCATTGCGATTCCACATGGCTGGGCGAC	2933
AAV-2	.....T....C.....A.....	2913
AAV-6	.....	2918
AAV-1	AGAGTCATCACCACCAGCACCCGCACCTGGGCCTTGCCACCTACAATAACCACCTCTAC	2993
AAV-2	.....A.....C.....C.....	2973
AAV-6	.....A..A.....T..C.....	2978
AAV-1	AAGCAAATCTCCAGTGCTTCAACGGGGGCCAGCAACGACAACCACTACTTCGGCTACAGC	3053
AAV-2	..A.....T.....CCAA...---..A...TCG.....T.....T.....	3030
AAV-6	.....	3038
AAV-1	ACCCCTGGGGGTATTTTGATTTCACAGATTCCACTGCCACTTTTCACCACGTGACTGG	3113
AAV-2	.....T.....C.....	3090
AAV-6	.....T..C.....	3098
AAV-1	CAGCGACTCATCAACAACAATTGGGGATTCCGGCCCAAGAGACTCAACTTCAAACCTCTTC	3173
AAV-2	..AA.....C.....A.....G.....T	3150
AAV-6	.....G.....	3158
AAV-1	AACATCCAAGTCAAGGAGGTCACGACGAATGATGGCGTCACAACCATCGCTAATAACCTT	3233
AAV-2	.....T.....A.....CA.....C..TACG..G..G..T..C.....	3210
		3218

5/13

FIG 1E

AAV-1 ACCAGCACGGTTCAAGTCTTCTCGGACTCGGAGTACCAGCTTCCGTACGTCCTCGGCTCT 3293  
 AAV-2 .....G..G..TA.T.....C.....G 3270  
 AAV-6 .....T.G..... 3278

AAV-1 GCGCACCAGGGCTGCCTCCCTCCGTTCGGGCGGACGTGTTTCATGATTCCGCAATACGGC 3353  
 AAV-2 .....T..A..A.....G.....A..A....C.....G.G..A..G..T..A 3330  
 AAV-6 .....G..... 3338

AAV-1 TACCTGACGCTCAACAATGGCAGCCAAGCCGTGGGACGTTTCATCCTTTTACTGCCTGGAA 3413  
 AAV-2 .....C..C..G.....C..G..T..G..A..A....C..T..A.....G 3390  
 AAV-6 .....A.....G..A.....G..... 3398

AAV-1 TATTTCCCTTCTCAGATGCTGAGAACGGGCAACAACCTTTACCTTCAGCTACACCTTTGAG 3473  
 AAV-2 ..C..T.....C.T..C..A.....T..... 3450  
 AAV-6 .....A..G.....T.....C... 3458

AAV-1 GAAGTGCCTTTCCACAGCAGCTACGCGCACAGCCAGAGCCTGGACCGGCTGATGAATCCT 3533  
 AAV-2 ..C..T.....T.....T.....T..C..... 3510  
 AAV-6 ..C..... 3498

AAV-1 CTCATCGACCAATACCTGTATTACCTGAACAGAACTCAAATCAGTCCGGAAGTGCCCAA 3593  
 AAV-2 .....G.....T...G.....AA.C.C..CAAGT....CCA..ACG 3570  
 AAV-6 .....G.....G..... 3578

AAV-1 AACAAGGACTTGCTGTTTAGCCGTGGGTCTCCAGCTGGCATGTCTGTTTCAGCCCAAAAAC 3653  
 AAV-2 C.GTCAAGGC.T.A....TCT.AG.CCGGAG.GAG..A...TCGG.AC...T.T.GG... 3630  
 AAV-6 .....G..... 3638

AAV-1 TGGCTACCTGGACCCTGTTATCGGCAGCAGCGGTTTCTAAACAAAAACAGACAACAAC 3713  
 AAV-2 .....T.....C..C.....A..A.CA..G...TCTG.G..T..... 3690  
 AAV-6 .....C..... 3698

AAV-1 AACAGCAATTTTACCTGGACTGGTGCTTCAAATATAACCTCAATGGGCGTGAATCCATC 3773  
 AAV-2 .....TG.A.ACT.G.....A...A.C..G..CC.....CA.A..C..TC.G 3750  
 AAV-6 .....C.....T.....T..A 3758

AAV-1 ATCAACCCTGGCACTGCTATGGCCTCACACAAAGACGACGAAGACAAGTTCTTTCCCATG 3833  
 AAV-2 G.G..T..G..GC.C..C....AAGC.....G....T.....A.....T....TCA. 3810  
 AAV-6 .....A..... 3818

AAV-1 AGCGGTGTCATGATTTTTGGAAAAGAGAGCGCCGGAGCTTCAAACACTGCATTGGACAAT 3893  
 AAV-2 .....G..TC.C..C.....G..GC.AG..T.A.AGAAAA...TGTGAACA.T..A..G 3870  
 AAV-6 .....G..... 3878

AAV-1 GTCATGATTACAGACGAAGAGGAAATTAAAGCCACTAACCCTGTGGCCACCGAAAGATTT 3953  
 AAV-2 .....CGG.A.A..C..T..C.....T..G..GCAG.A. 3930  
 AAV-6 .....C.....C.....C..... 3938

AAV-1 GGGACCGTGGCAGTCAATTTCCAGAGCAGCAGCACAGACCCTGCGACCGGAGATGTGCAT 4013  
 AAV-2 ..TT.T..AT.TAC...CC.....AG...A..G.C.AG.A..T....C.....CA.C 3990  
 AAV-6 .....T.....C..... 3998

AAV-1 GCTATGGGAGCATTACCTGGCATGGTGTGGCAAGATAGAGACGTGTACCTGCAGGGTCCC 4073  
 AAV-2 A.ACAA..C.TTC.T..A.....C.....T.....T.....G... 4050  
 AAV-6 T.....C.....A.....C.....A.....T 4058

6/13

FIG 1F

AAV-1 ATTTGGGCCAAAATTCCTCACACAGATGGACACTTTCACCCGTCTCCTCTTATGGGCGGC 4133  
 AAV-2 ..C.....A..G.....A.....G..C.....T.....C.....C..C.....T..A 4110  
 AAV-6 .....G.....C..... 4118  
  
 AAV-1 TTTGGACTCAAGAACCCGCCTCCTCAGATCCTCATCAAAACACGCCTGTTCTCCTGCGAAT 4193  
 AAV-2 ..C.....T..AC....T.....A.....T.....G.....C..G..A..... 4170  
 AAV-6 .....T...C..... 4178  
  
 AAV-1 CCTCCGGCGGAGTTTTTCAGCTACAAAGTTTGCTTCATTCATCACCCAATACTCCACAGGA 4253  
 AAV-2 ...T..A.CACC..CAGT..GG.....C.....A..G.....G... 4230  
 AAV-6 .....A.....G.....G..T..... 4238  
  
 AAV-1 CA-AGTGAGTGTGGAAATTGAATGGGAGCTGCAGAAAGAAAACAGCAAGCGCTGGAATCC 4312  
 AAV-2 ..CG..C..C.....G..C..G.....G.....A..... 4290  
 AAV-6 ..-.....C.....G.....A..... 4297  
  
 AAV-1 CGAAGTGCAGTACACATCCAATTATGCAAAATCTGCCAA-CGTTGATTTTACTGTGGACA 4371  
 AAV-2 ....A.T.....T.....C..CAAC..G....TT..T...G..C.....C.....T. 4350  
 AAV-6 .....T.....T..C.....-.....C..... 4356  
  
 AAV-1 ACAATGGACTTTTATACTGAGCCTCGCCCCATTGGCACCCGTTACCTTACCCGTCCCCTGT 4431  
 AAV-2 CT.....CG.G...T.A.....A.A.....G..T...AAT.... 4410  
 AAV-6 .....C..... 4416  
  
 VP1-3 stop PolyA signal  
 AAV-1 AATTACGTGTTAATCAATAAACCGGTTGATTCGTTTCAGTTGAACTTTGGTCTCCTGTCC 4491  
 AAV-2 ....G.T.....T..A.....TGCGTA 4470  
 AAV-6 ....GT.....A.....G.....A....G 4476  
  
 AAV-1 TTCTTATCTTATC-GGTTACCATGGTTAT-AGCTTACACATTA--ACTGCTTGTTGCGC 4547  
 AAV-2 ..TC.T.....TA...T.....C..CGTAGA..AGT.GC.TGG.G.G..AA.CATTA 4530  
 AAV-6 ..A.....T...C.....A.CA.C-C.G.....--.....A..... 4533  
  
 AAV-1 TTCGCGATAAAAGACTTACGTCATCGGGttacccttagtgatggagttgcccactccctc 4607  
 AAV-2 ACTA.A.gg.a-----g..... 4570  
 AAV-6 .....at.----- 4572  
  
 AAV-1 tctgcgcgctcgctcgctcggtggggccggcagagcagagctctgccgtctgcggacctt 4667  
 AAV-2 .c.....ac..a.....gc..c..a..g..gc...a.gc.c.gg... 4630  
 AAV-6 .a.....g..... 4632  
  
 AAV-1 tgggtccgcaggccccaccgagcgcgagcgcgcgagagagggagtgggcaa 4718  
 AAV-2 ..cc.g.gc....t..gt.....c... 4681  
 AAV-6 .....t..... 4683



8/13

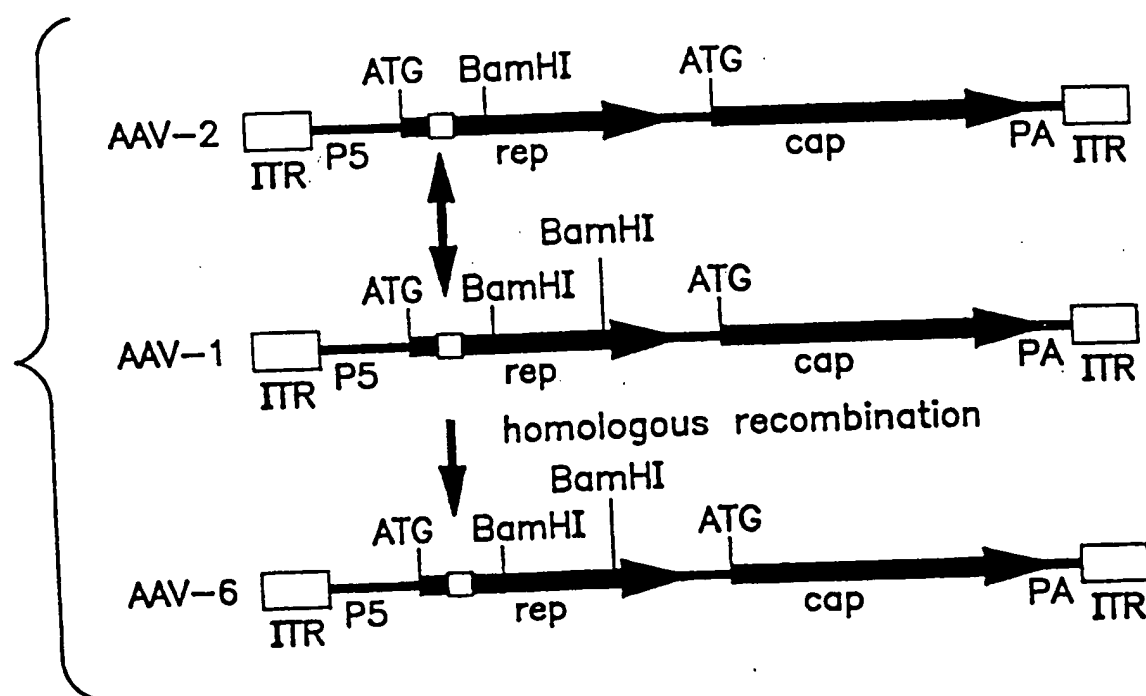


FIG. 3A



9/13

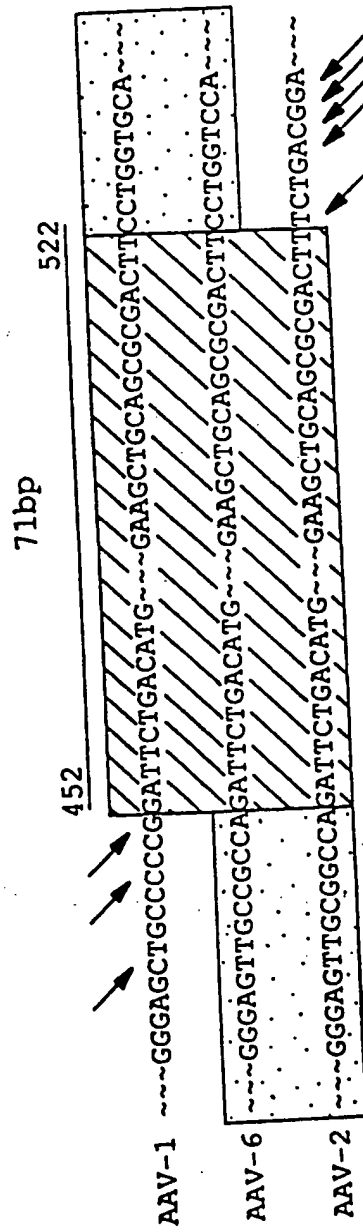


FIG. 3B

10/13

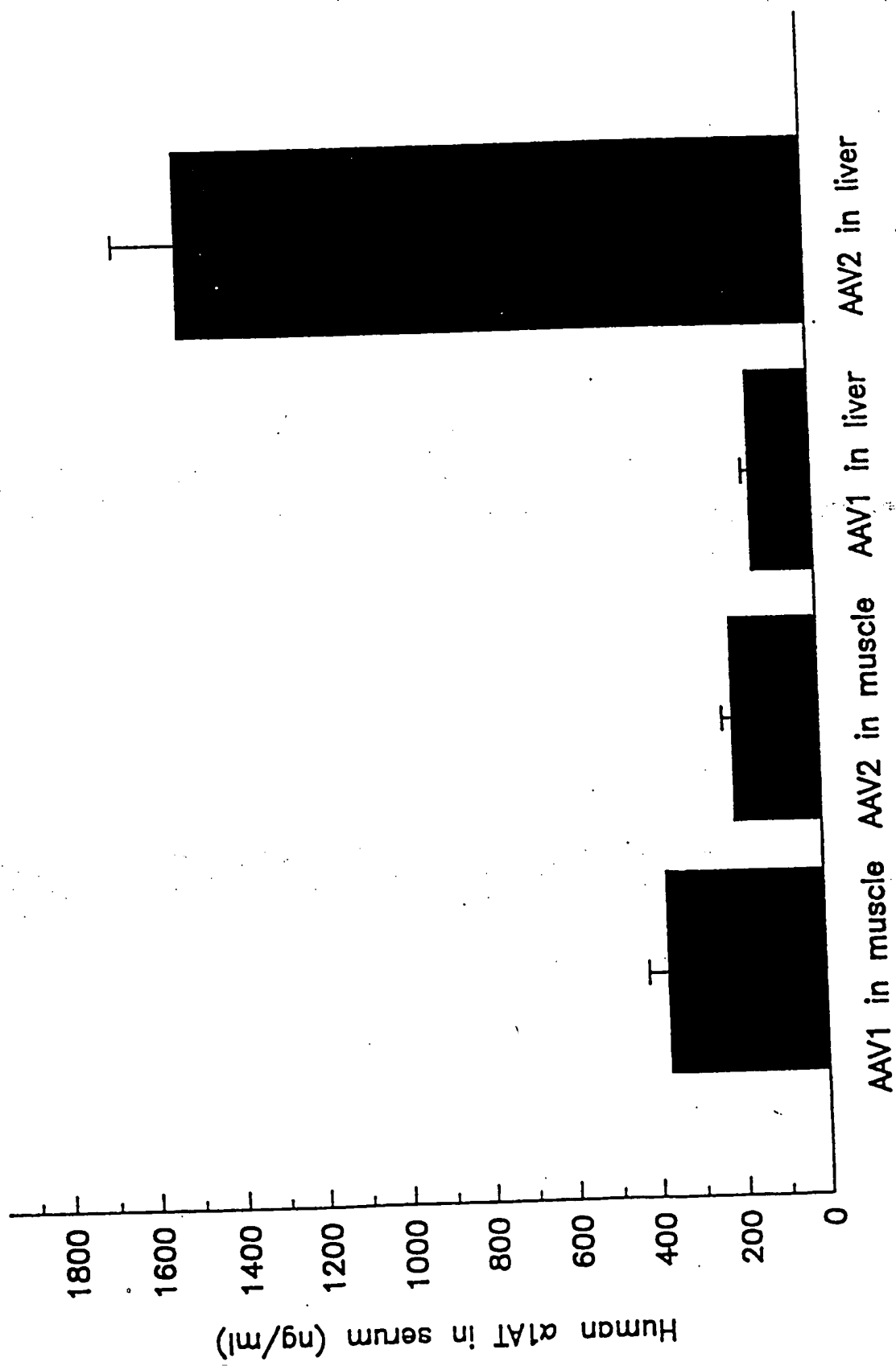


FIG. 4A

11/13

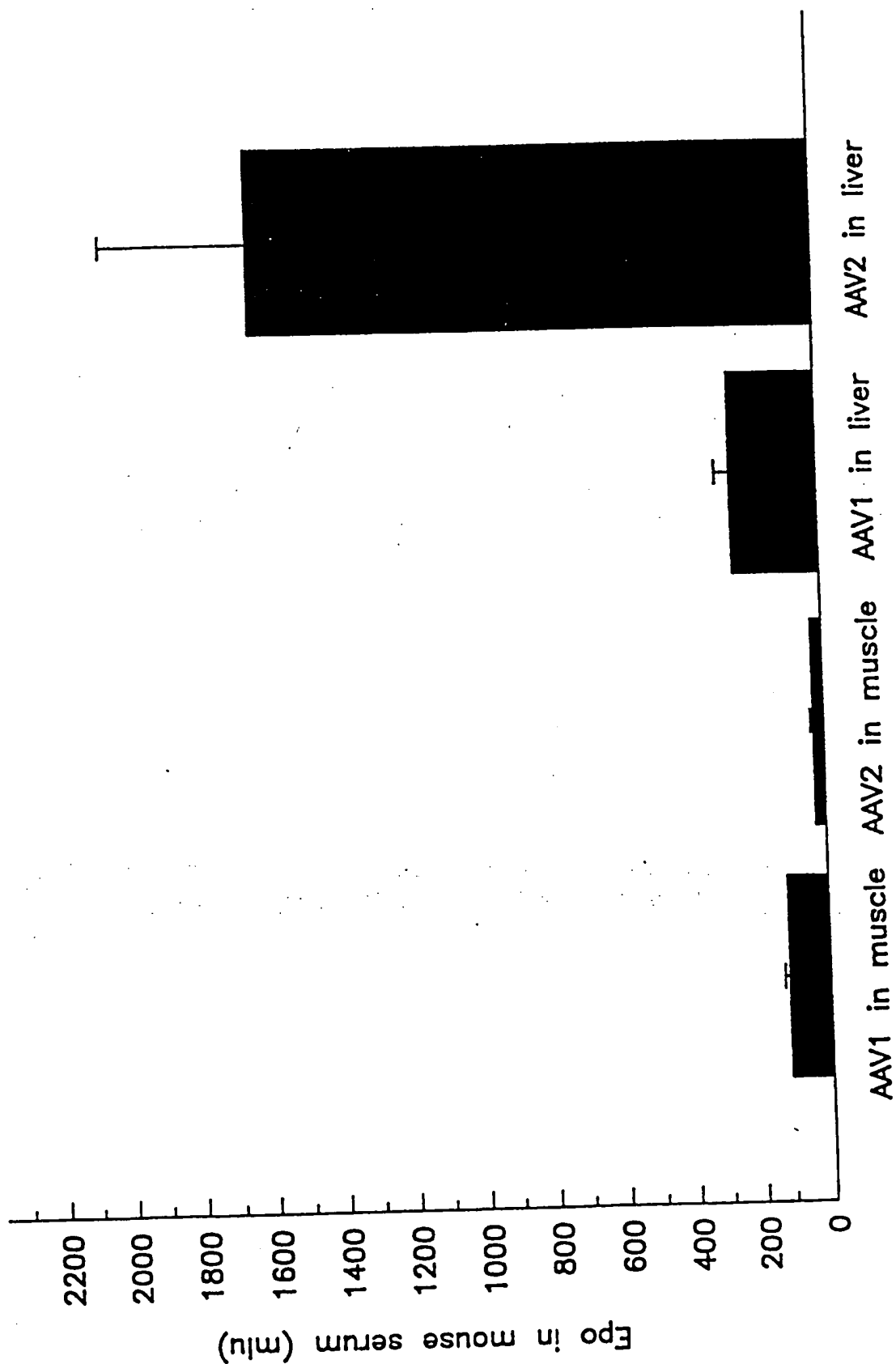


FIG. 4B

FIG. 5A

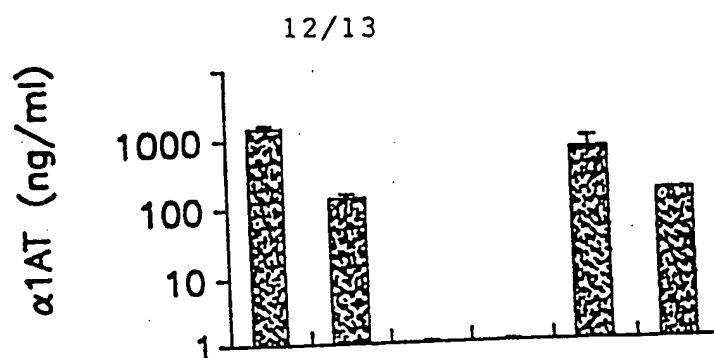


FIG. 5B

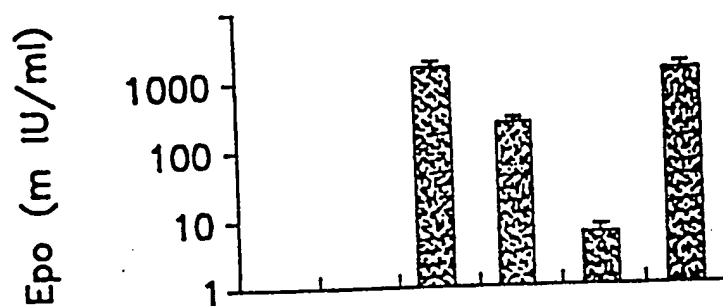


FIG. 5C

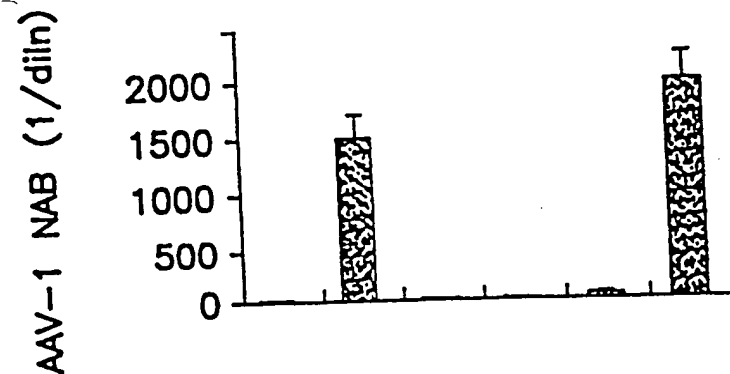
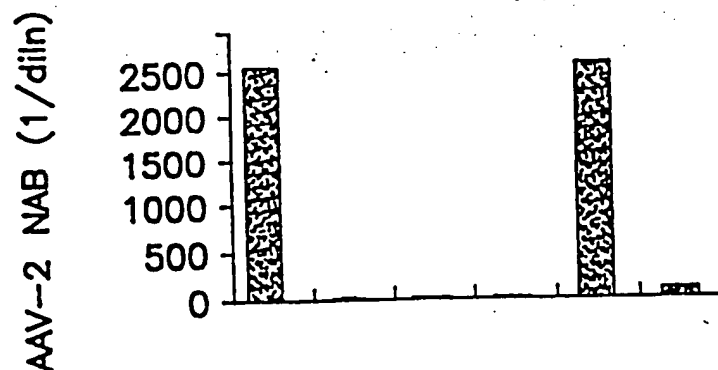


FIG. 5D



Group	1	2	3	4	5	6
Vector1- $\alpha 1AT$	AAV2	AAV1	PBS	PBS	AAV2	AAV1
Vector2-FPO	AAV2	AAV1	AAV2	AAV1	AAV1	AAV2

13/13

FIG. 6A

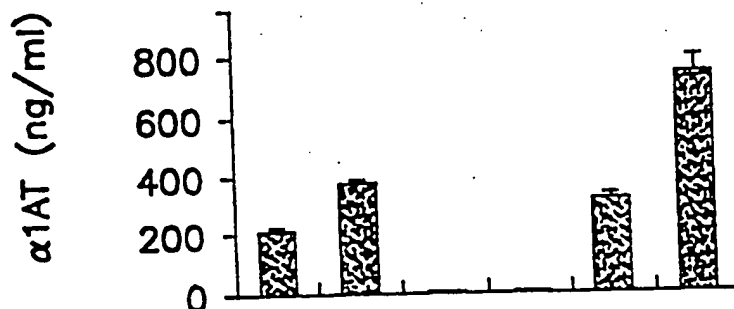


FIG. 6B

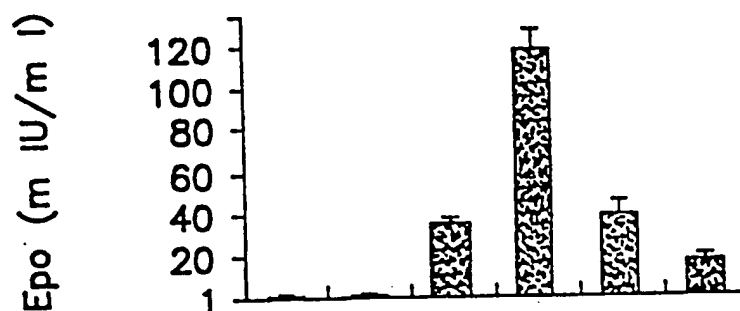


FIG. 6C

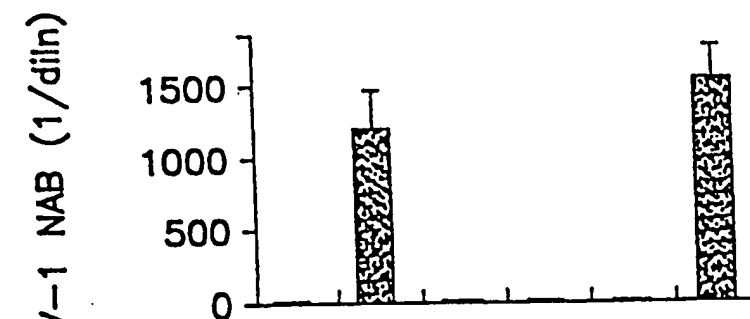
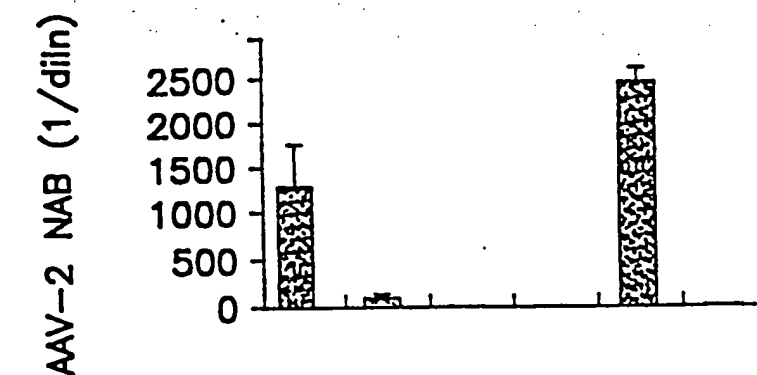


FIG. 6D



Group	1	2	3	4	5	6
Vector1- $\alpha$ 1AT	AAV2	AAV1	PBS	PBS	AAV2	AAV1
Vector2-EPO	AAV2	AAV1	AAV2	AAV1	AAV1	AAV2

## SEQUENCE LISTING

<110> Wilson, James M.  
Xiao, Weidong  
The Trustees of the University of Pennsylvania

<120> Adeno-Associated Virus Serotype I Nucleic Acid  
Sequences, Vectors and Host Cells Containing Same

<130> GNVPN.031PCT

<140>  
<141>

<150> 60/107,114  
<151> 1998-11-05

<160> 20

<170> PatentIn Ver. 2.0

<210> 1  
<211> 4718  
<212> DNA  
<213> AAV-1

<220>  
<221> CDS  
<222> (335)..(2206)

<220>  
<221> CDS  
<222> (2223)..(4430)

<400> 1  
ttgcccactc cctctctgcg cgctcgctcg ctcggtgggg cctgcggacc aaaggtccgc 60  
agacggcaga gctctgctct gccggcccca ccgagcgagc gagcgcgagc agagggagtg 120  
ggcaactcca tcactagggg taatcgcgaa gcgcctccca cgctgccgcg tcagcgctga 180  
cgtaaattac gtcatagggg agtggctctg tattagctgt cacgtgagtg cttttgcgac 240  
attttgcgac accacgtggc catttagggg atatatggcc gagtgagcga gcaggatctc 300  
cattttgacc gcgaaatttg aacgagcagc agcc atg ccg ggc ttc tac gag atc 355  
Met Pro Gly Phe Tyr Glu Ile

gtg atc aag gtg ccg agc gac ctg gac gag cac ctg ccg ggc att tct 403  
 Val Ile Lys Val Pro Ser Asp Leu Asp Glu His Leu Pro Gly Ile Ser  
 10 15 20

gac tcg ttt gtg agc tgg gtg gcc gag aag gaa tgg gag ctg ccc ccg 451  
 Asp Ser Phe Val Ser Trp Val Ala Glu Lys Glu Trp Glu Leu Pro Pro  
 25 30 35

gat tct gac atg gat ctg aat ctg att gag cag gca ccc ctg acc gtg 499  
 Asp Ser Asp Met Asp Leu Asn Leu Ile Glu Gln Ala Pro Leu Thr Val  
 40 45 50 55

gcc gag aag ctg cag cgc gac ttc ctg gtc caa tgg cgc cgc gtg agt 547  
 Ala Glu Lys Leu Gln Arg Asp Phe Leu Val Gln Trp Arg Arg Val Ser  
 60 65 70

aag gcc ccg gag gcc ctc ttc ttt gtt cag ttc gag aag ggc gag tcc 595  
 Lys Ala Pro Glu Ala Leu Phe Phe Val Gln Phe Glu Lys Gly Glu Ser  
 75 80 85

tac ttc cac ctc cat att ctg gtg gag acc acg ggg gtc aaa tcc atg 643  
 Tyr Phe His Leu His Ile Leu Val Glu Thr Thr Gly Val Lys Ser Met  
 90 95 100

gtg ctg ggc cgc ttc ctg agt cag att agg gac aag ctg gtg cag acc 691  
 Val Leu Gly Arg Phe Leu Ser Gln Ile Arg Asp Lys Leu Val Gln Thr  
 105 110 115

atc tac cgc ggg atc gag ccg acc ctg ccc aac tgg ttc gcg gtg acc 739  
 Ile Tyr Arg Gly Ile Glu Pro Thr Leu Pro Asn Trp Phe Ala Val Thr  
 120 125 130 135

aag acg cgt aat ggc gcc gga ggg ggg aac aag gtg gtg gac gag tgc 787  
 Lys Thr Arg Asn Gly Ala Gly Gly Gly Asn Lys Val Val Asp Glu Cys  
 140 145 150

tac atc ccc aac tac ctc ctg ccc aag act cag ccc gag ctg cag tgg 835  
 Tyr Ile Pro Asn Tyr Leu Leu Pro Lys Thr Gln Pro Glu Leu Gln Trp  
 155 160 165

gcg tgg act aac atg gag gag tat ata agc gcc tgt ttg aac ctg gcc 883  
 Ala Trp Thr Asn Met Glu Glu Tyr Ile Ser Ala Cys Leu Asn Leu Ala  
 170 175 180

gag cgc aaa cgg ctc gtg gcg cag cac ctg acc cac gtc agc cag acc 931  
 Glu Arg Lys Arg Leu Val Ala Gln His Leu Thr His Val Ser Gln Thr  
 185 190 195

cag gag cag aac aag gag aat ctg aac ccc aat tct gac gcg cct gtc 979  
 Gln Glu Gln Asn Lys Glu Asn Leu Asn Pro Asn Ser Asp Ala Pro Val  
 200 205 210 215

atc cgg tca aaa acc tcc gcg cgc tac atg gag ctg gtc ggg tgg ctg 1027  
 Ile Arg Ser Lys Thr Ser Ala Arg Tyr Met Glu Leu Val Gly Trp Leu  
 220 225 230

gtg gac cgg ggc atc acc tcc gag aag cag tgg atc cag gag gac cag 1075  
 Val Asp Arg Gly Ile Thr Ser Glu Lys Gln Trp Ile Gln Glu Asp Gln  
 235 240 245

gcc tcg tac atc tcc ttc aac gcc gct tcc aac tcg cgg tcc cag atc 1123  
 Ala Ser Tyr Ile Ser Phe Asn Ala Ala Ser Asn Ser Arg Ser Gln Ile  
 250 255 260

aag gcc gct ctg gac aat gcc ggc aag atc atg gcg ctg acc aaa tcc 1171  
 Lys Ala Ala Leu Asp Asn Ala Gly Lys Ile Met Ala Leu Thr Lys Ser  
 265 270 275

gcg ccc gac tac ctg gta ggc ccc gct ccg ccc gcg gac att aaa acc 1219  
 Ala Pro Asp Tyr Leu Val Gly Pro Ala Pro Pro Ala Asp Ile Lys Thr  
 280 285 290 295

aac cgc atc tac cgc atc ctg gag ctg aac ggc tac gaa cct gcc tac 1267  
 Asn Arg Ile Tyr Arg Ile Leu Glu Leu Asn Gly Tyr Glu Pro Ala Tyr  
 300 305 310

gcc ggc tcc gtc ttt ctc ggc tgg gcc cag aaa agg ttc ggg aag cgc 1315  
 Ala Gly Ser Val Phe Leu Gly Trp Ala Gln Lys Arg Phe Gly Lys Arg  
 315 320 325

aac acc atc tgg ctg ttt ggg ccg gcc acc acg ggc aag acc aac atc 1363  
 Asn Thr Ile Trp Leu Phe Gly Pro Ala Thr Thr Gly Lys Thr Asn Ile  
 330 335 340

gcg gaa gcc atc gcc cac gcc gtg ccc ttc tac ggc tgc gtc aac tgg 1411  
 Ala Glu Ala Ile Ala His Ala Val Pro Phe Tyr Gly Cys Val Asn Trp  
 345 350 355

acc aat gag aac ttt ccc ttc aat gat tgc gtc gac aag atg gtg atc 1459  
 Thr Asn Glu Asn Phe Pro Phe Asn Asp Cys Val Asp Lys Met Val Ile  
 360 365 370 375

tgg tgg gag gag ggc aag atg acg gcc aag gtc gtg gag tcc gcc aag 1507  
 Trp Trp Glu Glu Gly Lys Met Thr Ala Lys Val Val Glu Ser Ala Lys  
 380 385 390



```

gcc att ctc ggc ggc agc aag gtg cgc gtg gac caa aag tgc aag tcg      1555
Ala Ile Leu Gly Gly Ser Lys Val Arg Val Asp Gln Lys Cys Lys Ser
          395                      400                      405

tcc gcc cag atc gac ccc acc ccc gtg atc gtc acc tcc aac acc aac      1603
Ser Ala Gln Ile Asp Pro Thr Pro Val Ile Val Thr Ser Asn Thr Asn
          410                      415                      420

atg tgc gcc gtg att gac ggg aac agc acc acc ttc gag cac cag cag      1651
Met Cys Ala Val Ile Asp Gly Asn Ser Thr Thr Phe Glu His Gln Gln
          425                      430                      435

ccg ttg cag gac cgg atg ttc aaa ttt gaa ctc acc cgc cgt ctg gag      1699
Pro Leu Gln Asp Arg Met Phe Lys Phe Glu Leu Thr Arg Arg Leu Glu
          440                      445                      450                      455

cat gac ttt ggc aag gtg aca aag cag gaa gtc aaa gag ttc ttc cgc      1747
His Asp Phe Gly Lys Val Thr Lys Gln Glu Val Lys Glu Phe Phe Arg
          460                      465                      470

tgg gcg cag gat cac gtg acc gag gtg gcg cat gag ttc tac gtc aga      1795
Trp Ala Gln Asp His Val Thr Glu Val Ala His Glu Phe Tyr Val Arg
          475                      480                      485

aag ggt gga gcc aac aaa aga ccc gcc ccc gat gac gcg gat aaa agc      1843
Lys Gly Gly Ala Asn Lys Arg Pro Ala Pro Asp Asp Ala Asp Lys Ser
          490                      495                      500

gag ccc aag cgg gcc tgc ccc tca gtc gcg gat cca tcg acg tca gac      1891
Glu Pro Lys Arg Ala Cys Pro Ser Val Ala Asp Pro Ser Thr Ser Asp
          505                      510                      515

gcg gaa gga gct ccg gtg gac ttt gcc gac agg tac caa aac aaa tgt      1939
Ala Glu Gly Ala Pro Val Asp Phe Ala Asp Arg Tyr Gln Asn Lys Cys
          520                      525                      530                      535

tct cgt cac gcg ggc atg ctt cag atg ctg ttt ccc tgc aag aca tgc      1987
Ser Arg His Ala Gly Met Leu Gln Met Leu Phe Pro Cys Lys Thr Cys
          540                      545                      550

gag aga atg aat cag aat ttc aac att tgc ttc acg cac ggg acg aga      2035
Glu Arg Met Asn Gln Asn Phe Asn Ile Cys Phe Thr His Gly Thr Arg
          555                      560                      565

gac tgt tca gag tgc ttc ccc ggc gtg tca gaa tct caa ccg gtc gtc      2083
Asp Cys Ser Glu Cys Phe Pro Gly Val Ser Glu Ser Gln Pro Val Val
          570                      575                      580

```

aga aag agg acg tat cgg aaa ctc tgt gcc att cat cat ctg ctg ggg 2131  
 Arg Lys Arg Thr Tyr Arg Lys Leu Cys Ala Ile His His Leu Leu Gly  
 585 590 595

cgg gct ccc gag att gct tgc tcg gcc tgc gat ctg gtc aac gtg gac 2179  
 Arg Ala Pro Glu Ile Ala Cys Ser Ala Cys Asp Leu Val Asn Val Asp  
 600 605 610 615

ctg gat gac tgt gtt tct gag caa taa atgacttaaa ccaggt atg gct gcc 2231  
 Leu Asp Asp Cys Val Ser Glu Gln Met Ala Ala  
 620 625

gat ggt tat ctt cca gat tgg ctc gag gac aac ctc tct gag ggc att 2279  
 Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser Glu Gly Ile  
 630 635 640

cgc gag tgg tgg gac ttg aaa cct gga gcc ccg aag ccc aaa gcc aac 2327  
 Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro Lys Ala Asn  
 645 650 655

cag caa aag cag gac gac ggc cgg ggt ctg gtg ctt cct ggc tac aag 2375  
 Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro Gly Tyr Lys  
 660 665 670 675

tac ctc gga ccc ttc aac gga ctc gac aag ggg gag ccc gtc aac gcg 2423  
 Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro Val Asn Ala  
 680 685 690

gcg gac gca gcg gcc ctc gag cac gac aag gcc tac gac cag cag ctc 2471  
 Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp Gln Gln Leu  
 695 700 705

aaa gcg ggt gac aat ccg tac ctg cgg tat aac cac gcc gac gcc gag 2519  
 Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala Asp Ala Glu  
 710 715 720

ttt cag gag cgt ctg caa gaa gat acg tct ttt ggg ggc aac ctc ggg 2567  
 Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly Asn Leu Gly  
 725 730 735

cga gca gtc ttc cag gcc aag aag cgg gtt ctc gaa cct ctc ggt ctg 2615  
 Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Leu Gly Leu  
 740 745 750 755

gtt gag gaa ggc gct aag acg gct cct gga aag aaa cgt ccg gta gag 2663  
 Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg Pro Val Glu  
 760 765 770

cag tgc cca caa gag cca gac tcc tcc tgc ggc atc ggc aag aca ggc	2711
Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly Lys Thr Gly	
775 780 785	
cag cag ccc gct aaa aag aga ctc aat ttt ggt cag act ggc gac tca	2759
Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr Gly Asp Ser	
790 795 800	
gag tca gtc ccc gat cca caa cct ctc gga gaa cct cca gca acc ccc	2807
Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Thr Pro	
805 810 815	
gct gct gtg gga cct act aca atg gct tca ggc ggt ggc gca cca atg	2855
Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly Ala Pro Met	
820 825 830 835	
gca gac aat aac gaa ggc gcc gac gga gtg ggt aat gcc tca gga aat	2903
Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn	
840 845 850	
tgg cat tgc gat tcc aca tgg ctg ggc gac aga gtc atc acc acc agc	2951
Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser	
855 860 865	
acc cgc acc tgg gcc ttg ccc acc tac aat aac cac ctc tac aag caa	2999
Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln	
870 875 880	
atc tcc agt gct tca acg ggg gcc agc aac gac aac cac tac ttc ggc	3047
Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His Tyr Phe Gly	
885 890 895	
tac agc acc ccc tgg ggg tat ttt gat ttc aac aga ttc cac tgc cac	3095
Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His	
900 905 910 915	
ttt tca cca cgt gac tgg cag cga ctc atc aac aac aat tgg gga ttc	3143
Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe	
920 925 930	
cgg ccc aag aga ctc aac ttc aaa ctc ttc aac atc caa gtc aag gag	3191
Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val Lys Glu	
935 940 945	
gtc acg acg aat gat ggc gtc aca acc atc gct aat aac ctt acc agc	3239
Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser	
950 955 960	

acg gtt caa gtc ttc tcg gac tcg gag tac cag ctt ccg tac gtc ctc	3287
Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu	
965 970 975	
ggc tct gcg cac cag ggc tgc ctc cct ccg ttc ccg gcg gac gtg ttc	3335
Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe	
980 985 990 995	
atg att ccg caa tac ggc tac ctg acg ctc aac aat ggc agc caa gcc	3383
Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ala	
1000 1005 1010	
gtg gga cgt tca tcc ttt tac tgc ctg gaa tat ttc cct tct cag atg	3431
Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met	
1015 1020 1025	
ctg aga acg ggc aac aac ttt acc ttc agc tac acc ttt gag gaa gtg	3479
Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu Glu Val	
1030 1035 1040	
cct ttc cac agc agc tac gcg cac agc cag agc ctg gac cgg ctg atg	3527
Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met	
1045 1050 1055	
aat cct ctc atc gac caa tac ctg tat tac ctg aac aga act caa aat	3575
Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr Gln Asn	
1060 1065 1070 1075	
cag tcc gga agt gcc caa aac aag gac ttg ctg ttt agc cgt ggg tct	3623
Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser Arg Gly Ser	
1080 1085 1090	
cca gct ggc atg tct gtt cag ccc aaa aac tgg cta cct gga ccc tgt	3671
Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro Gly Pro Cys	
1095 1100 1105	
tat cgg cag cag cgc gtt tct aaa aca aaa aca gac aac aac aac agc	3719
Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn Asn Asn Ser	
1110 1115 1120	
aat ttt acc tgg act ggt gct tca aaa tat aac ctc aat ggg cgt gaa	3767
Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn Gly Arg Glu	
1125 1130 1135	
tcc atc atc aac cct ggc act gct atg gcc tca cac aaa gac gac gaa	3815
Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys Asp Asp Glu	
1140 1145 1150 1155	

gac aag ttc ttt ccc atg agc ggt gtc atg att ttt gga aaa gag agc 3863  
 Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly Lys Glu Ser  
 1160 1165 1170

gcc gga gct tca aac act gca ttg gac aat gtc atg att aca gac gaa 3911  
 Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile Thr Asp Glu  
 1175 1180 1185

gag gaa att aaa gcc act aac cct gtg gcc acc gaa aga ttt ggg acc 3959  
 Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg Phe Gly Thr  
 1190 1195 1200

gtg gca gtc aat ttc cag agc agc agc aca gac cct gcg acc gga gat 4007  
 Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala Thr Gly Asp  
 1205 1210 1215

gtg cat gct atg gga gca tta cct ggc atg gtg tgg caa gat aga gac 4055  
 Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln Asp Arg Asp  
 1220 1225 1230 1235

gtg tac ctg cag ggt ccc att tgg gcc aaa att cct cac aca gat gga 4103  
 Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly  
 1240 1245 1250

cac ttt cac ccg tct cct ctt atg ggc ggc ttt gga ctc aag aac ccg 4151  
 His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys Asn Pro  
 1255 1260 1265

cct cct cag atc ctc atc aaa aac acg cct gtt cct gcg aat cct ccg 4199  
 Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro  
 1270 1275 1280

gcg gag ttt tca gct aca aag ttt gct tca ttc atc acc caa tac tcc 4247  
 Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser  
 1285 1290 1295

aca gga caa gtg agt gtg gaa att gaa tgg gag ctg cag aaa gaa aac 4295  
 Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn  
 1300 1305 1310 1315

agc aag cgc tgg aat ccc gaa gtg cag tac aca tcc aat tat gca aaa 4343  
 Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn Tyr Ala Lys  
 1320 1325 1330

tct gcc aac gtt gat ttt act gtg gac aac aat gga ctt tat act gag 4391  
 Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu Tyr Thr Glu  
 1335 1340 1345

```

cct cgc ccc att ggc acc cgt tac ctt acc cgt ccc ctg taattacgtg      4440
Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
      1350              1355              1360

ttaatcaata aaccggttga ttcgtttcag ttgaactttg gtctcctgtc cttcttatct 4500

tatcggttac catggttata gcttacacat taactgcttg gttgcgcttc gcgataaaaag 4560

acttacgtca tcgggttacc cctagtgatg gagttgcccc ctccctctct gcgcgctcgc 4620

tcgctcggtg gggcctgcgg accaaaggtc cgcagacggc agagctctgc tctgccggcc 4680

ccaccgagcg agcgagcgcg cagagagggg gtgggcaa                        4718

```

&lt;210&gt; 2

&lt;211&gt; 623

&lt;212&gt; PRT

&lt;213&gt; AAV-1

&lt;400&gt; 2

```

Met Pro Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
  1              5              10              15

Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Ser Trp Val Ala Glu
      20              25              30

Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
      35              40              45

Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
      50              55              60

Val Gln Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
      65              70              75              80

Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Leu His Ile Leu Val Glu
      85              90              95

Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
      100              105              110

Arg Asp Lys Leu Val Gln Thr Ile Tyr Arg Gly Ile Glu Pro Thr Leu
      115              120              125

Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
      130              135              140

```

Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160

Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Glu Tyr Ile  
 165 170 175

Ser Ala Cys Leu Asn Leu Ala Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190

Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Leu Asn  
 195 200 205

Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220

Met Glu Leu Val Gly Trp Leu Val Asp Arg Gly Ile Thr Ser Glu Lys  
 225 230 235 240

Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 245 250 255

Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 260 265 270

Ile Met Ala Leu Thr Lys Ser Ala Pro Asp Tyr Leu Val Gly Pro Ala  
 275 280 285

Pro Pro Ala Asp Ile Lys Thr Asn Arg Ile Tyr Arg Ile Leu Glu Leu  
 290 295 300

Asn Gly Tyr Glu Pro Ala Tyr Ala Gly Ser Val Phe Leu Gly Trp Ala  
 305 310 315 320

Gln Lys Arg Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 325 330 335

Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro  
 340 345 350

Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 355 360 365

Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 370 375 380

Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 385 390 395 400

Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 405 410 415  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 420 425 430  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 435 440 445  
 Glu Leu Thr Arg Arg Leu Glu His Asp Phe Gly Lys Val Thr Lys Gln  
 450 455 460  
 Glu Val Lys Glu Phe Phe Arg Trp Ala Gln Asp His Val Thr Glu Val  
 465 470 475 480  
 Ala His Glu Phe Tyr Val Arg Lys Gly Gly Ala Asn Lys Arg Pro Ala  
 485 490 495  
 Pro Asp Asp Ala Asp Lys Ser Glu Pro Lys Arg Ala Cys Pro Ser Val  
 500 505 510  
 Ala Asp Pro Ser Thr Ser Asp Ala Glu Gly Ala Pro Val Asp Phe Ala  
 515 520 525  
 Asp Arg Tyr Gln Asn Lys Cys Ser Arg His Ala Gly Met Leu Gln Met  
 530 535 540  
 Leu Phe Pro Cys Lys Thr Cys Glu Arg Met Asn Gln Asn Phe Asn Ile  
 545 550 555 560  
 Cys Phe Thr His Gly Thr Arg Asp Cys Ser Glu Cys Phe Pro Gly Val  
 565 570 575  
 Ser Glu Ser Gln Pro Val Val Arg Lys Arg Thr Tyr Arg Lys Leu Cys  
 580 585 590  
 Ala Ile His His Leu Leu Gly Arg Ala Pro Glu Ile Ala Cys Ser Ala  
 595 600 605  
 Cys Asp Leu Val Asn Val Asp Leu Asp Asp Cys Val Ser Glu Gln  
 610 615 620

&lt;210&gt; 3

&lt;211&gt; 736

&lt;212&gt; PRT

&lt;213&gt; AAV-1



&lt;400&gt; 3

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
 1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
 20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
 35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
 85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
 100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly  
 145 150 155 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr  
 165 170 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro  
 180 185 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly  
 195 200 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala  
 210 215 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile  
 225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu

-	245	250	255
Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asp His	260	265	270
Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe	275	280	285
His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn	290	295	300
Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln	305	310	315
Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn	325	330	335
Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro	340	345	350
Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala	355	360	365
Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly	370	375	380
Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro	385	390	395
Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe	405	410	415
Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp	420	425	430
Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg	435	440	445
Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser	450	455	460
Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro	465	470	475
Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn	485	490	495
Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn			

	500		505		510	
Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys	515		520		525	
Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly	530		535		540	
Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile	545		550		555	560
Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg		565		570		575
Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala		580		585		590
Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln		595		600		605
Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His		610		615		620
Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu		625		630		635
						640
Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala		645		650		655
Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr		660		665		670
Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln		675		680		685
Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn		690		695		700
Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu		705		710		715
						720
Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu		725		730		735

&lt;210&gt; 4

&lt;211&gt; 1872

&lt;212&gt; DNA

&lt;213&gt; AAV-1

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1869)

&lt;400&gt; 4

atg ccg ggc ttc tac gag atc gtg atc aag gtg ccg agc gac ctg gac	48
Met Pro Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp	
1 5 10 15	
 gag cac ctg ccg ggc att tct gac tcg ttt gtg agc tgg gtg gcc gag	96
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Ser Trp Val Ala Glu	
20 25 30	
 aag gaa tgg gag ctg ccc ccg gat tct gac atg gat ctg aat ctg att	144
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile	
35 40 45	
 gag cag gca ccc ctg acc gtg gcc gag aag ctg cag cgc gac ttc ctg	192
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu	
50 55 60	
 gtc caa tgg cgc cgc gtg agt aag gcc ccg gag gcc ctc ttc ttt gtt	240
Val Gln Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val	
65 70 75 80	
 cag ttc gag aag ggc gag tcc tac ttc cac ctc cat att ctg gtg gag	288
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Leu His Ile Leu Val Glu	
85 90 95	
 acc acg ggg gtc aaa tcc atg gtg ctg ggc cgc ttc ctg agt cag att	336
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile	
100 105 110	
 agg gac aag ctg gtg cag acc atc tac cgc ggc atc gag ccg acc ctg	384
Arg Asp Lys Leu Val Gln Thr Ile Tyr Arg Gly Ile Glu Pro Thr Leu	
115 120 125	
 ccc aac tgg ttc gcg gtg acc aag acg cgt aat ggc gcc gga ggg ggg	432
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly	
130 135 140	
 aac aag gtg gtg gac gag tgc tac atc ccc aac tac ctc ctg ccc aag	480
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys	
145 150 155 160	
 act cag ccc gag ctg cag tgg gcg tgg act aac atg gag gag tat ata	528

Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Glu	Tyr	Ile	
				165					170					175		
agc	gcc	tgt	ttg	aac	ctg	gcc	gag	cgc	aaa	cgg	ctc	gtg	gcg	cag	cac	576
Ser	Ala	Cys	Leu	Asn	Leu	Ala	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His	
			180					185					190			
ctg	acc	cac	gtc	agc	cag	acc	cag	gag	cag	aac	aag	gag	aat	ctg	aac	624
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Leu	Asn	
			195				200					205				
ccc	aat	tct	gac	gcg	cct	gtc	atc	cgg	tca	aaa	acc	tcc	gcg	cgc	tac	672
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr	
	210					215				220						
atg	gag	ctg	gtc	ggg	tgg	ctg	gtg	gac	cgg	ggc	atc	acc	tcc	gag	aag	720
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Arg	Gly	Ile	Thr	Ser	Glu	Lys	
225				230				235						240		
cag	tgg	atc	cag	gag	gac	cag	gcc	tcg	tac	atc	tcc	ttc	aac	gcc	gct	768
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala	
			245					250					255			
tcc	aac	tcg	cgg	tcc	cag	atc	aag	gcc	gct	ctg	gac	aat	gcc	ggc	aag	816
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys	
			260				265					270				
atc	atg	gcg	ctg	acc	aaa	tcc	gcg	ccc	gac	tac	ctg	gta	ggc	ccc	gct	864
Ile	Met	Ala	Leu	Thr	Lys	Ser	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Pro	Ala	
			275				280					285				
ccg	ccc	gcg	gac	att	aaa	acc	aac	cgc	atc	tac	cgc	atc	ctg	gag	ctg	912
Pro	Pro	Ala	Asp	Ile	Lys	Thr	Asn	Arg	Ile	Tyr	Arg	Ile	Leu	Glu	Leu	
			290				295				300					
aac	ggc	tac	gaa	cct	gcc	tac	gcc	ggc	tcc	gtc	ttt	ctc	ggc	tgg	gcc	960
Asn	Gly	Tyr	Glu	Pro	Ala	Tyr	Ala	Gly	Ser	Val	Phe	Leu	Gly	Trp	Ala	
305				310						315				320		
cag	aaa	agg	ttc	ggg	aag	cgc	aac	acc	atc	tgg	ctg	ttt	ggg	ccg	gcc	1008
Gln	Lys	Arg	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala	
			325					330					335			
acc	acg	ggc	aag	acc	aac	atc	gcg	gaa	gcc	atc	gcc	cac	gcc	gtg	ccc	1056
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Ala	Val	Pro	
			340					345					350			
ttc	tac	ggc	tgc	gtc	aac	tgg	acc	aat	gag	aac	ttt	ccc	ttc	aat	gat	1104

Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp		
	355						360					365					
tgc	gtc	gac	aag	atg	gtg	atc	tgg	tgg	gag	gag	ggc	aag	atg	acg	gcc	1152	
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala		
	370					375					380						
aag	gtc	gtg	gag	tcc	gcc	aag	gcc	att	ctc	ggc	ggc	agc	aag	gtg	cgc	1200	
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg		
	385				390					395					400		
gtg	gac	caa	aag	tgc	aag	tcg	tcc	gcc	cag	atc	gac	ccc	acc	ccc	gtg	1248	
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val		
				405					410					415			
atc	gtc	acc	tcc	aac	acc	aac	atg	tgc	gcc	gtg	att	gac	ggg	aac	agc	1296	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser		
			420					425					430				
acc	acc	ttc	gag	cac	cag	cag	ccg	ttg	cag	gac	cgg	atg	ttc	aaa	ttt	1344	
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe		
		435					440					445					
gaa	ctc	acc	cgc	cgt	ctg	gag	cat	gac	ttt	ggc	aag	gtg	aca	aag	cag	1392	
Glu	Leu	Thr	Arg	Arg	Leu	Glu	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln		
	450					455					460						
gaa	gtc	aaa	gag	ttc	ttc	cgc	tgg	gcg	cag	gat	cac	gtg	acc	gag	gtg	1440	
Glu	Val	Lys	Glu	Phe	Phe	Arg	Trp	Ala	Gln	Asp	His	Val	Thr	Glu	Val		
	465					470				475					480		
gcg	cat	gag	ttc	tac	gtc	aga	aag	ggt	gga	gcc	aac	aaa	aga	ccc	gcc	1488	
Ala	His	Glu	Phe	Tyr	Val	Arg	Lys	Gly	Gly	Ala	Asn	Lys	Arg	Pro	Ala		
				485					490					495			
ccc	gat	gac	gcg	gat	aaa	agc	gag	ccc	aag	cgg	gcc	tgc	ccc	tca	gtc	1536	
Pro	Asp	Asp	Ala	Asp	Lys	Ser	Glu	Pro	Lys	Arg	Ala	Cys	Pro	Ser	Val		
			500					505					510				
gcg	gat	cca	tcg	acg	tca	gac	gcg	gaa	gga	gct	ccg	gtg	gac	ttt	gcc	1584	
Ala	Asp	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Gly	Ala	Pro	Val	Asp	Phe	Ala		
		515					520					525					
gac	agg	tac	caa	aac	aaa	tgt	tct	cgt	cac	gcg	ggc	atg	ctt	cag	atg	1632	
Asp	Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Ala	Gly	Met	Leu	Gln	Met		
	530					535					540						
ctg	ttt	ccc	tgc	aag	aca	tgc	gag	aga	atg	aat	cag	aat	ttc	aac	att	1680	

Leu Phe Pro Cys Lys Thr Cys Glu Arg Met Asn Gln Asn Phe Asn Ile  
 545 550 555 560

tgc ttc acg cac ggg acg aga gac tgt tca gag tgc ttc ccc ggc gtg 1728  
 Cys Phe Thr His Gly Thr Arg Asp Cys Ser Glu Cys Phe Pro Gly Val  
 565 570 575

tca gaa tct caa ccg gtc gtc aga aag agg acg tat cgg aaa ctc tgt 1776  
 Ser Glu Ser Gln Pro Val Val Arg Lys Arg Thr Tyr Arg Lys Leu Cys  
 580 585 590

gcc att cat cat ctg ctg ggg cgg gct ccc gag att gct tgc tcg gcc 1824  
 Ala Ile His His Leu Leu Gly Arg Ala Pro Glu Ile Ala Cys Ser Ala  
 595 600 605

tgc gat ctg gtc aac gtg gac ctg gat gac tgt gtt tct gag caa taa 1872  
 Cys Asp Leu Val Asn Val Asp Leu Asp Asp Cys Val Ser Glu Gln  
 610 615 620

<210> 5  
 <211> 623  
 <212> PRT  
 <213> AAV-1

<400> 5  
 Met Pro Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15

Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Ser Trp Val Ala Glu  
 20 25 30

Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45

Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60

Val Gln Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80

Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Leu His Ile Leu Val Glu  
 85 90 95

Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110

Arg Asp Lys Leu Val Gln Thr Ile Tyr Arg Gly Ile Glu Pro Thr Leu

115	120	125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly		
130	135	140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys		
145	150	155
		160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Glu Tyr Ile		
	165	170
		175
Ser Ala Cys Leu Asn Leu Ala Glu Arg Lys Arg Leu Val Ala Gln His		
	180	185
		190
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Leu Asn		
195	200	205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr		
210	215	220
Met Glu Leu Val Gly Trp Leu Val Asp Arg Gly Ile Thr Ser Glu Lys		
225	230	235
		240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala		
	245	250
		255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys		
	260	265
		270
Ile Met Ala Leu Thr Lys Ser Ala Pro Asp Tyr Leu Val Gly Pro Ala		
275	280	285
Pro Pro Ala Asp Ile Lys Thr Asn Arg Ile Tyr Arg Ile Leu Glu Leu		
290	295	300
Asn Gly Tyr Glu Pro Ala Tyr Ala Gly Ser Val Phe Leu Gly Trp Ala		
305	310	315
		320
Gln Lys Arg Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala		
	325	330
		335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro		
340	345	350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp		
355	360	365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala		



- 370

375

380

Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 385 390 395 400

Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 405 410 415

Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 420 425 430

Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 435 440 445

Glu Leu Thr Arg Arg Leu Glu His Asp Phe Gly Lys Val Thr Lys Gln  
 450 455 460

Glu Val Lys Glu Phe Phe Arg Trp Ala Gln Asp His Val Thr Glu Val  
 465 470 475 480

Ala His Glu Phe Tyr Val Arg Lys Gly Gly Ala Asn Lys Arg Pro Ala  
 485 490 495

Pro Asp Asp Ala Asp Lys Ser Glu Pro Lys Arg Ala Cys Pro Ser Val  
 500 505 510

Ala Asp Pro Ser Thr Ser Asp Ala Glu Gly Ala Pro Val Asp Phe Ala  
 515 520 525

Asp Arg Tyr Gln Asn Lys Cys Ser Arg His Ala Gly Met Leu Gln Met  
 530 535 540

Leu Phe Pro Cys Lys Thr Cys Glu Arg Met Asn Gln Asn Phe Asn Ile  
 545 550 555 560

Cys Phe Thr His Gly Thr Arg Asp Cys Ser Glu Cys Phe Pro Gly Val  
 565 570 575

Ser Glu Ser Gln Pro Val Val Arg Lys Arg Thr Tyr Arg Lys Leu Cys  
 580 585 590

Ala Ile His His Leu Leu Gly Arg Ala Pro Glu Ile Ala Cys Ser Ala  
 595 600 605

Cys Asp Leu Val Asn Val Asp Leu Asp Asp Cys Val Ser Glu Gln  
 610 615 620

&lt;210&gt; 6

&lt;211&gt; 1641

&lt;212&gt; DNA

&lt;213&gt; AAV-1

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1638)

&lt;400&gt; 6

atg	ccg	ggc	ttc	tac	gag	atc	gtg	atc	aag	gtg	ccg	agc	gac	ctg	gac	48
Met	Pro	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp	
1				5					10					15		

gag	cac	ctg	ccg	ggc	att	tct	gac	tcg	ttt	gtg	agc	tgg	gtg	gcc	gag	96
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Ser	Trp	Val	Ala	Glu	
			20					25					30			

aag	gaa	tgg	gag	ctg	ccc	ccg	gat	tct	gac	atg	gat	ctg	aat	ctg	att	144
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile	
		35					40					45				

gag	cag	gca	ccc	ctg	acc	gtg	gcc	gag	aag	ctg	cag	cgc	gac	ttc	ctg	192
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu	
		50				55					60					

gtc	caa	tgg	cgc	cgc	gtg	agt	aag	gcc	ccg	gag	gcc	ctc	ttc	ttt	gtt	240
Val	Gln	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val	
65					70					75					80	

cag	ttc	gag	aag	ggc	gag	tcc	tac	ttc	cac	ctc	cat	att	ctg	gtg	gag	288
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Leu	His	Ile	Leu	Val	Glu	
				85					90					95		

acc	acg	ggg	gtc	aaa	tcc	atg	gtg	ctg	ggc	cgc	ttc	ctg	agt	cag	att	336
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile	
			100					105					110			

agg	gac	aag	ctg	gtg	cag	acc	atc	tac	cgc	ggg	atc	gag	ccg	acc	ctg	384
Arg	Asp	Lys	Leu	Val	Gln	Thr	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu	
		115				120						125				

ccc	aac	tgg	ttc	gcg	gtg	acc	aag	acg	cgt	aat	ggc	gcc	gga	ggg	ggg	432
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly	
		130				135					140					

aac	aag	gtg	gtg	gac	gag	tgc	tac	atc	ccc	aac	tac	ctc	ctg	ccc	aag	480
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys	

145	150	155	160	
act cag ccc gag ctg	cag tgg gcg tgg	act aac atg gag	gag tat ata	528
Thr Gln Pro Glu Leu	Gln Trp Ala Trp	Thr Asn Met Glu	Glu Tyr Ile	
	165	170	175	
agc gcc tgt ttg aac	ctg gcc gag cgc	aaa cgg ctc gtg	gcg cag cac	576
Ser Ala Cys Leu Asn	Leu Ala Glu Arg	Lys Arg Leu Val	Ala Gln His	
	180	185	190	
ctg acc cac gtc agc	cag acc cag gag	cag aac aag gag	aat ctg aac	624
Leu Thr His Val Ser	Gln Thr Gln Glu	Gln Asn Lys Glu	Asn Leu Asn	
	195	200	205	
ccc aat tct gac gcg	cct gtc atc cgg	tca aaa acc tcc	gcg cgc tac	672
Pro Asn Ser Asp Ala	Pro Val Ile Arg	Ser Lys Thr Ser	Ala Arg Tyr	
	210	215	220	
atg gag ctg gtc ggg	tgg ctg gtg gac	cgg ggc atc acc	tcc gag aag	720
Met Glu Leu Val Gly	Trp Leu Val Asp	Arg Gly Ile Thr	Ser Glu Lys	
225	230	235	240	
cag tgg atc cag gag	gac cag gcc tcg	tac atc tcc ttc	aac gcc gct	768
Gln Trp Ile Gln Glu	Asp Gln Ala Ser	Tyr Ile Ser Phe	Asn Ala Ala	
	245	250	255	
tcc aac tcg cgg tcc	cag atc aag gcc	gct ctg gac aat	gcc ggc aag	816
Ser Asn Ser Arg Ser	Gln Ile Lys Ala	Ala Leu Asp Asn	Ala Gly Lys	
	260	265	270	
atc atg gcg ctg acc	aaa tcc gcg ccc	gac tac ctg gta	ggc ccc gct	864
Ile Met Ala Leu Thr	Lys Ser Ala Pro	Asp Tyr Leu Val	Gly Pro Ala	
	275	280	285	
ccg ccc gcg gac att	aaa acc aac cgc	atc tac cgc atc	ctg gag ctg	912
Pro Pro Ala Asp Ile	Lys Thr Asn Arg	Ile Tyr Arg Ile	Leu Glu Leu	
	290	295	300	
aac ggc tac gaa cct	gcc tac gcc ggc	tcc gtc ttt ctc	ggc tgg gcc	960
Asn Gly Tyr Glu Pro	Ala Tyr Ala Gly	Ser Val Phe Leu	Gly Trp Ala	
305	310	315	320	
cag aaa agg ttc ggg	aag cgc aac acc	atc tgg ctg ttt	ggg ccg gcc	1008
Gln Lys Arg Phe Gly	Lys Arg Asn Thr	Ile Trp Leu Phe	Gly Pro Ala	
	325	330	335	
acc acg ggc aag acc	aac atc gcg gaa	gcc atc gcc cac	gcc gtg ccc	1056
Thr Thr Gly Lys Thr	Asn Ile Ala Glu	Ala Ile Ala His	Ala Val Pro	

-	340	345	350	
ttc tac ggc tgc gtc aac tgg acc aat gag aac ttt ccc ttc aat gat				1104
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp				
355	360	365		
tgc gtc gac aag atg gtg atc tgg tgg gag gag ggc aag atg acg gcc				1152
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala				
370	375	380		
aag gtc gtg gag tcc gcc aag gcc att ctc ggc ggc agc aag gtg cgc				1200
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg				
385	390	395	400	
gtg gac caa aag tgc aag tcg tcc gcc cag atc gac ccc acc ccc gtg				1248
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val				
405	410	415		
atc gtc acc tcc aac acc aac atg tgc gcc gtg att gac ggg aac agc				1296
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser				
420	425	430		
acc acc ttc gag cac cag cag ccg ttg cag gac cgg atg ttc aaa ttt				1344
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe				
435	440	445		
gaa ctc acc cgc cgt ctg gag cat gac ttt ggc aag gtg aca aag cag				1392
Glu Leu Thr Arg Arg Leu Glu His Asp Phe Gly Lys Val Thr Lys Gln				
450	455	460		
gaa gtc aaa gag ttc ttc cgc tgg gcg cag gat cac gtg acc gag gtg				1440
Glu Val Lys Glu Phe Phe Arg Trp Ala Gln Asp His Val Thr Glu Val				
465	470	475	480	
gcg cat gag ttc tac gtc aga aag ggt gga gcc aac aaa aga ccc gcc				1488
Ala His Glu Phe Tyr Val Arg Lys Gly Gly Ala Asn Lys Arg Pro Ala				
485	490	495		
ccc gat gac gcg gat aaa agc gag ccc aag cgg gcc tgc ccc tca gtc				1536
Pro Asp Asp Ala Asp Lys Ser Glu Pro Lys Arg Ala Cys Pro Ser Val				
500	505	510		
gcg gat cca tcg acg tca gac gcg gaa gga gct ccg gtg gac ttt gcc				1584
Ala Asp Pro Ser Thr Ser Asp Ala Glu Gly Ala Pro Val Asp Phe Ala				
515	520	525		
gac agg tat ggc tgc cga tgg tta tct tcc aga ttg gct cga gga caa				1632
Asp Arg Tyr Gly Cys Arg Trp Leu Ser Ser Arg Leu Ala Arg Gly Gln				

- 530

535

540

cct ctc tga

1641

Pro Leu

545

&lt;210&gt; 7

&lt;211&gt; 546

&lt;212&gt; PRT

&lt;213&gt; AAV-1

&lt;400&gt; 7

Met Pro Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15

Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Ser Trp Val Ala Glu  
 20 25 30

Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45

Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60

Val Gln Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80

Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Leu His Ile Leu Val Glu  
 85 90 95

Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110

Arg Asp Lys Leu Val Gln Thr Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
 115 120 125

Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140

Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160

Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Glu Tyr Ile  
 165 170 175

Ser Ala Cys Leu Asn Leu Ala Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190

Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Leu Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Arg Gly Ile Thr Ser Glu Lys  
 225 230 235 240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 245 250 255  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 260 265 270  
 Ile Met Ala Leu Thr Lys Ser Ala Pro Asp Tyr Leu Val Gly Pro Ala  
 275 280 285  
 Pro Pro Ala Asp Ile Lys Thr Asn Arg Ile Tyr Arg Ile Leu Glu Leu  
 290 295 300  
 Asn Gly Tyr Glu Pro Ala Tyr Ala Gly Ser Val Phe Leu Gly Trp Ala  
 305 310 315 320  
 Gln Lys Arg Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 325 330 335  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro  
 340 345 350  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 355 360 365  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 370 375 380  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 385 390 395 400  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 405 410 415  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 420 425 430  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 435 440 445

Glu Leu Thr Arg Arg Leu Glu His Asp Phe Gly Lys Val Thr Lys Gln  
 450 455 460

Glu Val Lys Glu Phe Phe Arg Trp Ala Gln Asp His Val Thr Glu Val  
 465 470 475 480

Ala His Glu Phe Tyr Val Arg Lys Gly Gly Ala Asn Lys Arg Pro Ala  
 485 490 495

Pro Asp Asp Ala Asp Lys Ser Glu Pro Lys Arg Ala Cys Pro Ser Val  
 500 505 510

Ala Asp Pro Ser Thr Ser Asp Ala Glu Gly Ala Pro Val Asp Phe Ala  
 515 520 525

Asp Arg Tyr Gly Cys Arg Trp Leu Ser Ser Arg Leu Ala Arg Gly Gln  
 530 535 540

Pro Leu  
 545

<210> 8

<211> 1200

<212> DNA

<213> AAV-1

<220>

<221> CDS

<222> (1)..(1197)

<400> 8

atg gag ctg gtc ggg tgg ctg gtg gac cgg ggc atc acc tcc gag aag 48  
 Met Glu Leu Val Gly Trp Leu Val Asp Arg Gly Ile Thr Ser Glu Lys  
 1 5 10 15

cag tgg atc cag gag gac cag gcc tcg tac atc tcc ttc aac gcc gct 96  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 20 25 30

tcc aac tcg cgg tcc cag atc aag gcc gct ctg gac aat gcc ggc aag 144  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 35 40 45

atc atg gcg ctg acc aaa tcc gcg ccc gac tac ctg gta ggc ccc gct 192  
 Ile Met Ala Leu Thr Lys Ser Ala Pro Asp Tyr Leu Val Gly Pro Ala  
 50 55 60

```

ccg ccc gcg gac att aaa acc aac cgc atc tac cgc atc ctg gag ctg      240
Pro Pro Ala Asp Ile Lys Thr Asn Arg Ile Tyr Arg Ile Leu Glu Leu
 65              70              75              80

aac ggc tac gaa cct gcc tac gcc ggc tcc gtc ttt ctc ggc tgg gcc      288
Asn Gly Tyr Glu Pro Ala Tyr Ala Gly Ser Val Phe Leu Gly Trp Ala
      85              90              95

cag aaa agg ttc ggg aag cgc aac acc atc tgg ctg ttt ggg ccg gcc      336
Gln Lys Arg Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      100              105              110

acc acg ggc aag acc aac atc gcg gaa gcc atc gcc cac gcc gtg ccc      384
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro
      115              120              125

ttc tac ggc tgc gtc aac tgg acc aat gag aac ttt ccc ttc aat gat      432
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      130              135              140

tgc gtc gac aag atg gtg atc tgg tgg gag gag ggc aag atg acg gcc      480
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
      145              150              155              160

aag gtc gtg gag tcc gcc aag gcc att ctc ggc ggc agc aag gtg cgc      528
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
      165              170              175

gtg gac caa aag tgc aag tcg tcc gcc cag atc gac ccc acc ccc gtg      576
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      180              185              190

atc gtc acc tcc aac acc aac atg tgc gcc gtg att gac ggg aac agc      624
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      195              200              205

acc acc ttc gag cac cag cag ccg ttg cag gac cgg atg ttc aaa ttt      672
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      210              215              220

gaa ctc acc cgc cgt ctg gag cat gac ttt ggc aag gtg aca aag cag      720
Glu Leu Thr Arg Arg Leu Glu His Asp Phe Gly Lys Val Thr Lys Gln
      225              230              235              240

gaa gtc aaa gag ttc ttc cgc tgg gcg cag gat cac gtg acc gag gtg      768
Glu Val Lys Glu Phe Phe Arg Trp Ala Gln Asp His Val Thr Glu Val
      245              250              255

```



gcg cat gag ttc tac gtc aga aag ggt gga gcc aac aaa aga ccc gcc 816  
 Ala His Glu Phe Tyr Val Arg Lys Gly Gly Ala Asn Lys Arg Pro Ala  
                   260                                  265                                  270

ccc gat gac gcg gat aaa agc gag ccc aag cgg gcc tgc ccc tca gtc 864  
 Pro Asp Asp Ala Asp Lys Ser Glu Pro Lys Arg Ala Cys Pro Ser Val  
                   275                                  280                                  285

gcg gat cca tcg acg tca gac gcg gaa gga gct ccg gtg gac ttt gcc 912  
 Ala Asp Pro Ser Thr Ser Asp Ala Glu Gly Ala Pro Val Asp Phe Ala  
                   290                                  295                                  300

gac agg tac caa aac aaa tgt tct cgt cac gcg ggc atg ctt cag atg 960  
 Asp Arg Tyr Gln Asn Lys Cys Ser Arg His Ala Gly Met Leu Gln Met  
 305                                  310                                  315                                  320

ctg ttt ccc tgc aag aca tgc gag aga atg aat cag aat ttc aac att 1008  
 Leu Phe Pro Cys Lys Thr Cys Glu Arg Met Asn Gln Asn Phe Asn Ile  
                                   325                                  330                                  335

tgc ttc acg cac ggg acg aga gac tgt tca gag tgc ttc ccc ggc gtg 1056  
 Cys Phe Thr His Gly Thr Arg Asp Cys Ser Glu Cys Phe Pro Gly Val  
                   340                                  345                                  350

tca gaa tct caa ccg gtc gtc aga aag agg acg tat cgg aaa ctc tgt 1104  
 Ser Glu Ser Gln Pro Val Val Arg Lys Arg Thr Tyr Arg Lys Leu Cys  
                   355                                  360                                  365

gcc att cat cat ctg ctg ggg cgg gct ccc gag att gct tgc tcg gcc 1152  
 Ala Ile His His Leu Leu Gly Arg Ala Pro Glu Ile Ala Cys Ser Ala  
                   370                                  375                                  380

tgc gat ctg gtc aac gtg gac ctg gat gac tgt gtt tct gag caa taa 1200  
 Cys Asp Leu Val Asn Val Asp Leu Asp Asp Cys Val Ser Glu Gln  
 385                                  390                                  395

<210> 9

<211> 399

<212> PRT

<213> AAV-1

<400> 9

Met Glu Leu Val Gly Trp Leu Val Asp Arg Gly Ile Thr Ser Glu Lys  
           1                                  5                                  10                                  15

Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala

	20		25		30	
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys	35		40		45	
Ile Met Ala Leu Thr Lys Ser Ala Pro Asp Tyr Leu Val Gly Pro Ala	50		55		60	
Pro Pro Ala Asp Ile Lys Thr Asn Arg Ile Tyr Arg Ile Leu Glu Leu	65		70		75	80
Asn Gly Tyr Glu Pro Ala Tyr Ala Gly Ser Val Phe Leu Gly Trp Ala		85		90		95
Gln Lys Arg Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala		100		105		110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro		115		120		125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp		130		135		140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala		145		150		155
						160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg		165		170		175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val		180		185		190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser		195		200		205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe		210		215		220
Glu Leu Thr Arg Arg Leu Glu His Asp Phe Gly Lys Val Thr Lys Gln		225		230		235
						240
Glu Val Lys Glu Phe Phe Arg Trp Ala Gln Asp His Val Thr Glu Val		245		250		255
Ala His Glu Phe Tyr Val Arg Lys Gly Gly Ala Asn Lys Arg Pro Ala		260		265		270
Pro Asp Asp Ala Asp Lys Ser Glu Pro Lys Arg Ala Cys Pro Ser Val						

275                                      280                                      285  
 Ala Asp Pro Ser Thr Ser Asp Ala Glu Gly Ala Pro Val Asp Phe Ala  
 290                                      295                                      300  
 Asp Arg Tyr Gln Asn Lys Cys Ser Arg His Ala Gly Met Leu Gln Met  
 305                                      310                                      315                                      320  
 Leu Phe Pro Cys Lys Thr Cys Glu Arg Met Asn Gln Asn Phe Asn Ile  
 325                                      330                                      335  
 Cys Phe Thr His Gly Thr Arg Asp Cys Ser Glu Cys Phe Pro Gly Val  
 340                                      345                                      350  
 Ser Glu Ser Gln Pro Val Val Arg Lys Arg Thr Tyr Arg Lys Leu Cys  
 355                                      360                                      365  
 Ala Ile His His Leu Leu Gly Arg Ala Pro Glu Ile Ala Cys Ser Ala  
 370                                      375                                      380  
 Cys Asp Leu Val Asn Val Asp Leu Asp Asp Cys Val Ser Glu Gln  
 385                                      390                                      395

&lt;210&gt; 10

&lt;211&gt; 969

&lt;212&gt; DNA

&lt;213&gt; AAV-1

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(966)

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (943)..(944)

&lt;223&gt; minor splice site

&lt;400&gt; 10

atg gag ctg gtc ggg tgg ctg gtg gac cgg ggc atc acc tcc gag aag 48  
 Met Glu Leu Val Gly Trp Leu Val Asp Arg Gly Ile Thr Ser Glu Lys  
 1                                      5                                      10                                      15

cag tgg atc cag gag gac cag gcc tcg tac atc tcc ttc aac gcc gct 96  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 20                                      25                                      30

tcc aac tcg cgg tcc cag atc aag gcc gct ctg gac aat gcc ggc aag 144

Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys	
	35						40					45				
atc	atg	gcg	ctg	acc	aaa	tcc	gcg	ccc	gac	tac	ctg	gta	ggc	ccc	gct	192
Ile	Met	Ala	Leu	Thr	Lys	Ser	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Pro	Ala	
	50					55					60					
ccg	ccc	gcg	gac	att	aaa	acc	aac	cgc	atc	tac	cgc	atc	ctg	gag	ctg	240
Pro	Pro	Ala	Asp	Ile	Lys	Thr	Asn	Arg	Ile	Tyr	Arg	Ile	Leu	Glu	Leu	
	65				70					75				80		
aac	ggc	tac	gaa	cct	gcc	tac	gcc	ggc	tcc	gtc	ttt	ctc	ggc	tgg	gcc	288
Asn	Gly	Tyr	Glu	Pro	Ala	Tyr	Ala	Gly	Ser	Val	Phe	Leu	Gly	Trp	Ala	
			85						90				95			
cag	aaa	agg	ttc	ggg	aag	cgc	aac	acc	atc	tgg	ctg	ttt	ggg	ccg	gcc	336
Gln	Lys	Arg	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala	
			100					105					110			
acc	acg	ggc	aag	acc	aac	atc	gcg	gaa	gcc	atc	gcc	cac	gcc	gtg	ccc	384
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Ala	Val	Pro	
		115					120					125				
ttc	tac	ggc	tgc	gtc	aac	tgg	acc	aat	gag	aac	ttt	ccc	ttc	aat	gat	432
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp	
	130					135					140					
tgc	gtc	gac	aag	atg	gtg	atc	tgg	tgg	gag	gag	ggc	aag	atg	acg	gcc	480
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala	
	145				150					155				160		
aag	gtc	gtg	gag	tcc	gcc	aag	gcc	att	ctc	ggc	ggc	agc	aag	gtg	cgc	528
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg	
			165						170				175			
gtg	gac	caa	aag	tgc	aag	tcg	tcc	gcc	cag	atc	gac	ccc	acc	ccc	gtg	576
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val	
			180					185					190			
atc	gtc	acc	tcc	aac	acc	aac	atg	tgc	gcc	gtg	att	gac	ggg	aac	agc	624
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser	
		195					200					205				
acc	acc	ttc	gag	cac	cag	cag	ccg	ttg	cag	gac	cgg	atg	ttc	aaa	ttt	672
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe	
		210				215					220					
gaa	ctc	acc	cgc	cgt	ctg	gag	cat	gac	ttt	ggc	aag	gtg	aca	aag	cag	720

Glu Leu Thr Arg Arg Leu Glu His Asp Phe Gly Lys Val Thr Lys Gln  
 225 230 235 240  
 gaa gtc aaa gag ttc ttc cgc tgg gcg cag gat cac gtg acc gag gtg 768  
 Glu Val Lys Glu Phe Phe Arg Trp Ala Gln Asp His Val Thr Glu Val  
 245 250 255  
 gcg cat gag ttc tac gtc aga aag ggt gga gcc aac aaa aga ccc gcc 816  
 Ala His Glu Phe Tyr Val Arg Lys Gly Gly Ala Asn Lys Arg Pro Ala  
 260 265 270  
 ccc gat gac gcg gat aaa agc gag ccc aag cgg gcc tgc ccc tca gtc 864  
 Pro Asp Asp Ala Asp Lys Ser Glu Pro Lys Arg Ala Cys Pro Ser Val  
 275 280 285  
 gcg gat cca tcg acg tca gac gcg gaa gga gct ccg gtg gac ttt gcc 912  
 Ala Asp Pro Ser Thr Ser Asp Ala Glu Gly Ala Pro Val Asp Phe Ala  
 290 295 300  
 gac agg tat ggc tgc cga tgg tta tct tcc aga ttg gct cga gga caa 960  
 Asp Arg Tyr Gly Cys Arg Trp Leu Ser Ser Arg Leu Ala Arg Gly Gln  
 305 310 315 320  
 cct ctc tga 969  
 Pro Leu

<210> 11  
 <211> 322  
 <212> PRT  
 <213> AAV-1

<400> 11  
 Met Glu Leu Val Gly Trp Leu Val Asp Arg Gly Ile Thr Ser Glu Lys  
 1 5 10 15  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 20 25 30  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 35 40 45  
 Ile Met Ala Leu Thr Lys Ser Ala Pro Asp Tyr Leu Val Gly Pro Ala  
 50 55 60  
 Pro Pro Ala Asp Ile Lys Thr Asn Arg Ile Tyr Arg Ile Leu Glu Leu  
 65 70 75 80

Asn Gly Tyr Glu Pro Ala Tyr Ala Gly Ser Val Phe Leu Gly Trp Ala  
                                     85                                    90                                    95

Gln Lys Arg Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
                                     100                                    105                                    110

Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro  
                                     115                                    120                                    125

Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
                                     130                                    135                                    140

Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
                                     145                                    150                                    155                                    160

Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
                                     165                                    170                                    175

Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
                                     180                                    185                                    190

Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
                                     195                                    200                                    205

Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
                                     210                                    215                                    220

Glu Leu Thr Arg Arg Leu Glu His Asp Phe Gly Lys Val Thr Lys Gln  
                                     225                                    230                                    235                                    240

Glu Val Lys Glu Phe Phe Arg Trp Ala Gln Asp His Val Thr Glu Val  
                                     245                                    250                                    255

Ala His Glu Phe Tyr Val Arg Lys Gly Gly Ala Asn Lys Arg Pro Ala  
                                     260                                    265                                    270

Pro Asp Asp Ala Asp Lys Ser Glu Pro Lys Arg Ala Cys Pro Ser Val  
                                     275                                    280                                    285

Ala Asp Pro Ser Thr Ser Asp Ala Glu Gly Ala Pro Val Asp Phe Ala  
                                     290                                    295                                    300

Asp Arg Tyr Gly Cys Arg Trp Leu Ser Ser Arg Leu Ala Arg Gly Gln  
                                     305                                    310                                    315                                    320

Pro Leu

&lt;210&gt; 12

&lt;211&gt; 2211

&lt;212&gt; DNA

&lt;213&gt; AAV-1

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(2208)

&lt;400&gt; 12

atg gct gcc gat ggt tat ctt cca gat tgg ctc gag gac aac ctc tct	48
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser	
1 5 10 15	
 gag ggc att cgc gag tgg tgg gac ttg aaa cct gga gcc ccg aag ccc	96
Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro	
20 25 30	
 aaa gcc aac cag caa aag cag gac gac ggc cgg ggt ctg gtg ctt cct	144
Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro	
35 40 45	
 ggc tac aag tac ctc gga ccc ttc aac gga ctc gac aag ggg gag ccc	192
Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro	
50 55 60	
 gtc aac gcg gcg gac gca gcg gcc ctc gag cac gac aag gcc tac gac	240
Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp	
65 70 75 80	
 cag cag ctc aaa gcg ggt gac aat ccg tac ctg cgg tat aac cac gcc	288
Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala	
85 90 95	
 gac gcc gag ttt cag gag cgt ctg caa gaa gat acg tct ttt ggg ggc	336
Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly	
100 105 110	
 aac ctc ggg cga gca gtc ttc cag gcc aag aag cgg gtt ctc gaa cct	384
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro	
115 120 125	
 ctc ggt ctg gtt gag gaa ggc gct aag acg gct cct gga aag aaa cgt	432
Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg	
130 135 140	
 ccg gta gag cag tcg cca caa gag cca gac tcc tcc tcg ggc atc ggc	480

Pro-Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly	
145	150 155 160
aag aca ggc cag cag ccc gct aaa aag aga ctc aat ttt ggt cag act	528
Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr	
165	170 175
ggc gac tca gag tca gtc ccc gat cca caa cct ctc gga gaa cct cca	576
Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro	
180	185 190
gca acc ccc gct gct gtg gga cct act aca atg gct tca ggc ggt ggc	624
Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly	
195	200 205
gca cca atg gca gac aat aac gaa ggc gcc gac gga gtg ggt aat gcc	672
Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala	
210	215 220
tca gga aat tgg cat tgc gat tcc aca tgg ctg ggc gac aga gtc atc	720
Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile	
225	230 235 240
acc acc agc acc cgc acc tgg gcc ttg ccc acc tac aat aac cac ctc	768
Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu	
245	250 255
tac aag caa atc tcc agt gct tca acg ggg gcc agc aac gac aac cac	816
Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His	
260	265 270
tac ttc ggc tac agc acc ccc tgg ggg tat ttt gat ttc aac aga ttc	864
Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe	
275	280 285
cac tgc cac ttt tca cca cgt gac tgg cag cga ctc atc aac aac aat	912
His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn	
290	295 300
tgg gga ttc cgg ccc aag aga ctc aac ttc aaa ctc ttc aac atc caa	960
Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln	
305	310 315 320
gtc aag gag gtc acg acg aat gat ggc gtc aca acc atc gct aat aac	1008
Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn	
325	330 335
ctt acc agc acg gtt caa gtc ttc tcg gac tcg gag tac cag ctt ccg	1056



Leu	Thr	Ser	Thr	Val	Gln	Val	Phe	Ser	Asp	Ser	Glu	Tyr	Gln	Leu	Pro		
				340				345					350				
tac	gtc	ctc	ggc	tct	gcg	cac	cag	ggc	tgc	ctc	cct	ccg	ttc	ccg	gcg	1104	
Tyr	Val	Leu	Gly	Ser	Ala	His	Gln	Gly	Cys	Leu	Pro	Pro	Phe	Pro	Ala		
		355					360					365					
gac	gtg	ttc	atg	att	ccg	caa	tac	ggc	tac	ctg	acg	ctc	aac	aat	ggc	1152	
Asp	Val	Phe	Met	Ile	Pro	Gln	Tyr	Gly	Tyr	Leu	Thr	Leu	Asn	Asn	Gly		
		370				375					380						
agc	caa	gcc	gtg	gga	cgt	tca	tcc	ttt	tac	tgc	ctg	gaa	tat	ttc	cct	1200	
Ser	Gln	Ala	Val	Gly	Arg	Ser	Ser	Phe	Tyr	Cys	Leu	Glu	Tyr	Phe	Pro		
385					390					395					400		
tct	cag	atg	ctg	aga	acg	ggc	aac	aac	ttt	acc	ttc	agc	tac	acc	ttt	1248	
Ser	Gln	Met	Leu	Arg	Thr	Gly	Asn	Asn	Phe	Thr	Phe	Ser	Tyr	Thr	Phe		
				405					410					415			
gag	gaa	gtg	cct	ttc	cac	agc	agc	tac	gcg	cac	agc	cag	agc	ctg	gac	1296	
Glu	Glu	Val	Pro	Phe	His	Ser	Ser	Tyr	Ala	His	Ser	Gln	Ser	Leu	Asp		
			420					425						430			
cgg	ctg	atg	aat	cct	ctc	atc	gac	caa	tac	ctg	tat	tac	ctg	aac	aga	1344	
Arg	Leu	Met	Asn	Pro	Leu	Ile	Asp	Gln	Tyr	Leu	Tyr	Tyr	Leu	Asn	Arg		
		435					440					445					
act	caa	aat	cag	tcc	gga	agt	gcc	caa	aac	aag	gac	ttg	ctg	ttt	agc	1392	
Thr	Gln	Asn	Gln	Ser	Gly	Ser	Ala	Gln	Asn	Lys	Asp	Leu	Leu	Phe	Ser		
		450				455					460						
cgt	ggg	tct	cca	gct	ggc	atg	tct	gtt	cag	ccc	aaa	aac	tgg	cta	cct	1440	
Arg	Gly	Ser	Pro	Ala	Gly	Met	Ser	Val	Gln	Pro	Lys	Asn	Trp	Leu	Pro		
465					470					475					480		
gga	ccc	tgt	tat	cgg	cag	cag	cgc	gtt	tct	aaa	aca	aaa	aca	gac	aac	1488	
Gly	Pro	Cys	Tyr	Arg	Gln	Gln	Arg	Val	Ser	Lys	Thr	Lys	Thr	Asp	Asn		
				485					490					495			
aac	aac	agc	aat	ttt	acc	tgg	act	ggt	gct	tca	aaa	tat	aac	ctc	aat	1536	
Asn	Asn	Ser	Asn	Phe	Thr	Trp	Thr	Gly	Ala	Ser	Lys	Tyr	Asn	Leu	Asn		
			500					505					510				
ggg	cgt	gaa	tcc	atc	atc	aac	cct	ggc	act	gct	atg	gcc	tca	cac	aaa	1584	
Gly	Arg	Glu	Ser	Ile	Ile	Asn	Pro	Gly	Thr	Ala	Met	Ala	Ser	His	Lys		
		515					520					525					
gac	gac	gaa	gac	aag	ttc	ttt	ccc	atg	agc	ggt	gtc	atg	att	ttt	gga	1632	

Asp	Asp	Glu	Asp	Lys	Phe	Phe	Pro	Met	Ser	Gly	Val	Met	Ile	Phe	Gly		
530						535					540						
aaa	gag	agc	gcc	gga	gct	tca	aac	act	gca	ttg	gac	aat	gtc	atg	att	1680	
Lys	Glu	Ser	Ala	Gly	Ala	Ser	Asn	Thr	Ala	Leu	Asp	Asn	Val	Met	Ile		
545					550					555					560		
aca	gac	gaa	gag	gaa	att	aaa	gcc	act	aac	cct	gtg	gcc	acc	gaa	aga	1728	
Thr	Asp	Glu	Glu	Glu	Ile	Lys	Ala	Thr	Asn	Pro	Val	Ala	Thr	Glu	Arg		
				565					570					575			
ttt	ggg	acc	gtg	gca	gtc	aat	ttc	cag	agc	agc	agc	aca	gac	cct	gcg	1776	
Phe	Gly	Thr	Val	Ala	Val	Asn	Phe	Gln	Ser	Ser	Ser	Thr	Asp	Pro	Ala		
			580					585					590				
acc	gga	gat	gtg	cat	gct	atg	gga	gca	tta	cct	ggc	atg	gtg	tgg	caa	1824	
Thr	Gly	Asp	Val	His	Ala	Met	Gly	Ala	Leu	Pro	Gly	Met	Val	Trp	Gln		
		595					600					605					
gat	aga	gac	gtg	tac	ctg	cag	ggc	ccc	att	tgg	gcc	aaa	att	cct	cac	1872	
Asp	Arg	Asp	Val	Tyr	Leu	Gln	Gly	Pro	Ile	Trp	Ala	Lys	Ile	Pro	His		
	610					615					620						
aca	gat	gga	cac	ttt	cac	ccg	tct	cct	ctt	atg	ggc	ggc	ttt	gga	ctc	1920	
Thr	Asp	Gly	His	Phe	His	Pro	Ser	Pro	Leu	Met	Gly	Gly	Phe	Gly	Leu		
625					630					635					640		
aag	aac	ccg	cct	cct	cag	atc	ctc	atc	aaa	aac	acg	cct	gtt	cct	gcg	1968	
Lys	Asn	Pro	Pro	Pro	Gln	Ile	Leu	Ile	Lys	Asn	Thr	Pro	Val	Pro	Ala		
				645					650					655			
aat	cct	ccg	gcg	gag	ttt	tca	gct	aca	aag	ttt	gct	tca	ttc	atc	acc	2016	
Asn	Pro	Pro	Ala	Glu	Phe	Ser	Ala	Thr	Lys	Phe	Ala	Ser	Phe	Ile	Thr		
			660					665					670				
caa	tac	tcc	aca	gga	caa	gtg	agt	gtg	gaa	att	gaa	tgg	gag	ctg	cag	2064	
Gln	Tyr	Ser	Thr	Gly	Gln	Val	Ser	Val	Glu	Ile	Glu	Trp	Glu	Leu	Gln		
		675					680					685					
aaa	gaa	aac	agc	aag	cgc	tgg	aat	ccc	gaa	gtg	cag	tac	aca	tcc	aat	2112	
Lys	Glu	Asn	Ser	Lys	Arg	Trp	Asn	Pro	Glu	Val	Gln	Tyr	Thr	Ser	Asn		
	690					695					700						
tat	gca	aaa	tct	gcc	aac	gtt	gat	ttt	act	gtg	gac	aac	aat	gga	ctt	2160	
Tyr	Ala	Lys	Ser	Ala	Asn	Val	Asp	Phe	Thr	Val	Asp	Asn	Asn	Gly	Leu		
705					710					715					720		
tat	act	gag	cct	cgc	ccc	att	ggc	acc	cgt	tac	ctt	acc	cgt	ccc	ctg	2208	

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu  
 725 730 735

taa

2211

&lt;210&gt; 13

&lt;211&gt; 736

&lt;212&gt; PRT

&lt;213&gt; AAV-1

&lt;400&gt; 13

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser  
 1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro  
 20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro  
 35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
 50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
 65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala  
 85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly  
 100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
 115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg  
 130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly  
 145 150 155 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr  
 165 170 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro  
 180 185 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly  
 195 200 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala  
 210 215 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile  
 225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
 245 250 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His  
 260 265 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe  
 275 280 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn  
 290 295 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln  
 305 310 315 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn  
 325 330 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro  
 340 345 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala  
 355 360 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly  
 370 375 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro  
 385 390 395 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe  
 405 410 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp  
 420 425 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg  
 435 440 445

Thr\_Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser  
 450 455 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro  
 465 470 475 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn  
 485 490 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn  
 500 505 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys  
 515 520 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly  
 530 535 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile  
 545 550 555 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg  
 565 570 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala  
 580 585 590

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln  
 595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His  
 610 615 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu  
 625 630 635 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala  
 645 650 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr  
 660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln  
 675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn  
 690 695 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu  
 705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu  
 725 730 735

<210> 14

<211> 1800

<212> DNA

<213> AAV-1

<220>

<221> CDS

<222> (1) .. (1797)

<400> 14

acg gct cct gga aag aaa cgt ccg gta gag cag tcg cca caa gag cca 48  
 Thr Ala Pro Gly Lys Lys Arg Pro Val Glu Gln Ser Pro Gln Glu Pro  
 1 5 10 15

gac tcc tcc tcg ggc atc ggc aag aca ggc cag cag ccc gct aaa aag 96  
 Asp Ser Ser Ser Gly Ile Gly Lys Thr Gly Gln Gln Pro Ala Lys Lys  
 20 25 30

aga ctc aat ttt ggt cag act ggc gac tca gag tca gtc ccc gat cca 144  
 Arg Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu Ser Val Pro Asp Pro  
 35 40 45

caa cct ctc gga gaa cct cca gca acc ccc gct gct gtg gga cct act 192  
 Gln Pro Leu Gly Glu Pro Pro Ala Thr Pro Ala Ala Val Gly Pro Thr  
 50 55 60

aca atg gct tca ggc ggt ggc gca cca atg gca gac aat aac gaa ggc 240  
 Thr Met Ala Ser Gly Gly Gly Ala Pro Met Ala Asp Asn Asn Glu Gly  
 65 70 75 80

gcc gac gga gtg ggt aat gcc tca gga aat tgg cat tgc gat tcc aca 288  
 Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp His Cys Asp Ser Thr  
 85 90 95

tgg ctg ggc gac aga gtc atc acc acc agc acc cgc acc tgg gcc ttg 336  
 Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu  
 100 105 110

ccc acc tac aat aac cac ctc tac aag caa atc tcc agt gct tca acg 384  
 Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile Ser Ser Ala Ser Thr  
 115 120 125

ggg gcc agc aac gac aac cac tac ttc ggc tac agc acc ccc tgg ggg	432
Gly Ala Ser Asn Asp Asn His Tyr Phe Gly Tyr Ser Thr Pro Trp Gly	
130 135 140	
tat ttt gat ttc aac aga ttc cac tgc cac ttt tca cca cgt gac tgg	480
Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp	
145 150 155 160	
cag cga ctc atc aac aac aat tgg gga ttc cgg ccc aag aga ctc aac	528
Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn	
165 170 175	
ttc aaa ctc ttc aac atc caa gtc aag gag gtc acg acg aat gat ggc	576
Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr Thr Asn Asp Gly	
180 185 190	
gtc aca acc atc gct aat aac ctt acc agc acg gtt caa gtc ttc tcg	624
Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Ser	
195 200 205	
gac tcg gag tac cag ctt ccg tac gtc ctc ggc tct gcg cac cag ggc	672
Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly	
210 215 220	
tgc ctc cct ccg ttc ccg gcg gac gtg ttc atg att ccg caa tac ggc	720
Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly	
225 230 235 240	
tac ctg acg ctc aac aat ggc agc caa gcc gtg gga cgt tca tcc ttt	768
Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe	
245 250 255	
tac tgc ctg gaa tat ttc cct tct cag atg ctg aga acg ggc aac aac	816
Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn	
260 265 270	
ttt acc ttc agc tac acc ttt gag gaa gtg cct ttc cac agc agc tac	864
Phe Thr Phe Ser Tyr Thr Phe Glu Glu Val Pro Phe His Ser Ser Tyr	
275 280 285	
gcg cac agc cag agc ctg gac cgg ctg atg aat cct ctc atc gac caa	912
Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln	
290 295 300	
tac ctg tat tac ctg aac aga act caa aat cag tcc gga agt gcc caa	960
Tyr Leu Tyr Tyr Leu Asn Arg Thr Gln Asn Gln Ser Gly Ser Ala Gln	
305 310 315 320	

aac aag gac ttg ctg ttt agc cgt ggg tct cca gct ggc atg tct gtt	1008
Asn Lys Asp Leu Leu Phe Ser Arg Gly Ser Pro Ala Gly Met Ser Val	
325 330 335	
cag ccc aaa aac tgg cta cct gga ccc tgt tat cgg cag cag cgc gtt	1056
Gln Pro Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val	
340 345 350	
tct aaa aca aaa aca gac aac aac aac agc aat ttt acc tgg act ggt	1104
Ser Lys Thr Lys Thr Asp Asn Asn Asn Ser Asn Phe Thr Trp Thr Gly	
355 360 365	
gct tca aaa tat aac ctc aat ggg cgt gaa tcc atc atc aac cct ggc	1152
Ala Ser Lys Tyr Asn Leu Asn Gly Arg Glu Ser Ile Ile Asn Pro Gly	
370 375 380	
act gct atg gcc tca cac aaa gac gac gaa gac aag ttc ttt ccc atg	1200
Thr Ala Met Ala Ser His Lys Asp Asp Glu Asp Lys Phe Phe Pro Met	
385 390 395 400	
agc ggt gtc atg att ttt gga aaa gag agc gcc gga gct tca aac act	1248
Ser Gly Val Met Ile Phe Gly Lys Glu Ser Ala Gly Ala Ser Asn Thr	
405 410 415	
gca ttg gac aat gtc atg att aca gac gaa gag gaa att aaa gcc act	1296
Ala Leu Asp Asn Val Met Ile Thr Asp Glu Glu Glu Ile Lys Ala Thr	
420 425 430	
aac cct gtg gcc acc gaa aga ttt ggg acc gtg gca gtc aat ttc cag	1344
Asn Pro Val Ala Thr Glu Arg Phe Gly Thr Val Ala Val Asn Phe Gln	
435 440 445	
agc agc agc aca gac cct gcg acc gga gat gtg cat gct atg gga gca	1392
Ser Ser Ser Thr Asp Pro Ala Thr Gly Asp Val His Ala Met Gly Ala	
450 455 460	
tta cct ggc atg gtg tgg caa gat aga gac gtg tac ctg cag ggt ccc	1440
Leu Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro	
465 470 475 480	
att tgg gcc aaa att cct cac aca gat gga cac ttt cac ccg tct cct	1488
Ile Trp Ala Lys Ile Pro His Thr Asp Gly His Phe His Pro Ser Pro	
485 490 495	
ctt atg ggc ggc ttt gga ctc aag aac ccg cct cct cag atc ctc atc	1536
Leu Met Gly Gly Phe Gly Leu Lys Asn Pro Pro Pro Gln Ile Leu Ile	
500 505 510	



aaa aac acg cct gtt cct gcg aat cct ccg gcg gag ttt tca gct aca 1584  
 Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Ala Glu Phe Ser Ala Thr  
           515                          520                          525

aag ttt gct tca ttc atc acc caa tac tcc aca gga caa gtg agt gtg 1632  
 Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val  
           530                          535                          540

gaa att gaa tgg gag ctg cag aaa gaa aac agc aag cgc tgg aat ccc 1680  
 Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro  
           545                          550                          555                          560

gaa gtg cag tac aca tcc aat tat gca aaa tct gcc aac gtt gat ttt 1728  
 Glu Val Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Ala Asn Val Asp Phe  
                                   565                                  570                                  575

act gtg gac aac aat gga ctt tat act gag cct cgc ccc att ggc acc 1776  
 Thr Val Asp Asn Asn Gly Leu Tyr Thr Glu Pro Arg Pro Ile Gly Thr  
                                   580                                  585                                  590

cgt tac ctt acc cgt ccc ctg taa 1800  
 Arg Tyr Leu Thr Arg Pro Leu  
                                   595

<210> 15  
 <211> 599  
 <212> PRT  
 <213> AAV-1

<400> 15  
 Thr Ala Pro Gly Lys Lys Arg Pro Val Glu Gln Ser Pro Gln Glu Pro  
       1                          5                          10                          15

Asp Ser Ser Ser Gly Ile Gly Lys Thr Gly Gln Gln Pro Ala Lys Lys  
                           20                          25                          30

Arg Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu Ser Val Pro Asp Pro  
           35                          40                          45

Gln Pro Leu Gly Glu Pro Pro Ala Thr Pro Ala Ala Val Gly Pro Thr  
           50                          55                          60

Thr Met Ala Ser Gly Gly Gly Ala Pro Met Ala Asp Asn Asn Glu Gly  
       65                          70                          75                          80

Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp His Cys Asp Ser Thr

	85	90	95
Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu	100	105	110
Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile Ser Ser Ala Ser Thr	115	120	125
Gly Ala Ser Asn Asp Asn His Tyr Phe Gly Tyr Ser Thr Pro Trp Gly	130	135	140
Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp	145	150	155
Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn	165	170	175
Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr Thr Asn Asp Gly	180	185	190
Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Ser	195	200	205
Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly	210	215	220
Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly	225	230	235
Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe	245	250	255
Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn	260	265	270
Phe Thr Phe Ser Tyr Thr Phe Glu Glu Val Pro Phe His Ser Ser Tyr	275	280	285
Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln	290	295	300
Tyr Leu Tyr Tyr Leu Asn Arg Thr Gln Asn Gln Ser Gly Ser Ala Gln	305	310	315
Asn Lys Asp Leu Leu Phe Ser Arg Gly Ser Pro Ala Gly Met Ser Val	325	330	335
Gln Pro Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val			

-	340	345	350
Ser Lys Thr Lys Thr Asp Asn Asn Asn Ser Asn Phe Thr Trp Thr Gly	355	360	365
Ala Ser Lys Tyr Asn Leu Asn Gly Arg Glu Ser Ile Ile Asn Pro Gly	370	375	380
Thr Ala Met Ala Ser His Lys Asp Asp Glu Asp Lys Phe Phe Pro Met	385	390	395
Ser Gly Val Met Ile Phe Gly Lys Glu Ser Ala Gly Ala Ser Asn Thr	405	410	415
Ala Leu Asp Asn Val Met Ile Thr Asp Glu Glu Glu Ile Lys Ala Thr	420	425	430
Asn Pro Val Ala Thr Glu Arg Phe Gly Thr Val Ala Val Asn Phe Gln	435	440	445
Ser Ser Ser Thr Asp Pro Ala Thr Gly Asp Val His Ala Met Gly Ala	450	455	460
Leu Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro	465	470	475
Ile Trp Ala Lys Ile Pro His Thr Asp Gly His Phe His Pro Ser Pro	485	490	495
Leu Met Gly Gly Phe Gly Leu Lys Asn Pro Pro Pro Gln Ile Leu Ile	500	505	510
Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Ala Glu Phe Ser Ala Thr	515	520	525
Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val	530	535	540
Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro	545	550	555
Glu Val Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Ala Asn Val Asp Phe	565	570	575
Thr Val Asp Asn Asn Gly Leu Tyr Thr Glu Pro Arg Pro Ile Gly Thr	580	585	590
Arg Tyr Leu Thr Arg Pro Leu			

- 595

&lt;210&gt; 16

&lt;211&gt; 1605

&lt;212&gt; DNA

&lt;213&gt; AAV-1

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1602)

&lt;400&gt; 16

atg gct tca ggc ggt ggc gca cca atg gca gac aat aac gaa ggc gcc 48  
 Met Ala Ser Gly Gly Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala  
           1                  5                  10                  15

gac gga gtg ggt aat gcc tca gga aat tgg cat tgc gat tcc aca tgg 96  
 Asp Gly Val Gly Asn Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp  
                   20                  25                  30

ctg ggc gac aga gtc atc acc acc agc acc cgc acc tgg gcc ttg ccc 144  
 Leu Gly Asp Arg Val Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro  
                   35                  40                  45

acc tac aat aac cac ctc tac aag caa atc tcc agt gct tca acg ggg 192  
 Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly  
                   50                  55                  60

gcc agc aac gac aac cac tac ttc ggc tac agc acc ccc tgg ggg tat 240  
 Ala Ser Asn Asp Asn His Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr  
                   65                  70                  75                  80

ttt gat ttc aac aga ttc cac tgc cac ttt tca cca cgt gac tgg cag 288  
 Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln  
                   85                  90                  95

cga ctc atc aac aac aat tgg gga ttc cgg ccc aag aga ctc aac ttc 336  
 Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe  
                   100                  105                  110

aaa ctc ttc aac atc caa gtc aag gag gtc acg acg aat gat ggc gtc 384  
 Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val  
                   115                  120                  125

aca acc atc gct aat aac ctt acc agc acg gtt caa gtc ttc tcg gac 432  
 Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp  
                   130                  135                  140

tcg	gag	tac	cag	ctt	ccg	tac	gtc	ctc	ggc	tct	gcg	cac	cag	ggc	tgc	480
Ser	Glu	Tyr	Gln	Leu	Pro	Tyr	Val	Leu	Gly	Ser	Ala	His	Gln	Gly	Cys	
145					150					155					160	
ctc	cct	ccg	ttc	ccg	gcg	gac	gtg	ttc	atg	att	ccg	caa	tac	ggc	tac	528
Leu	Pro	Pro	Phe	Pro	Ala	Asp	Val	Phe	Met	Ile	Pro	Gln	Tyr	Gly	Tyr	
				165					170						175	
ctg	acg	ctc	aac	aat	ggc	agc	caa	gcc	gtg	gga	cgt	tca	tcc	ttt	tac	576
Leu	Thr	Leu	Asn	Asn	Gly	Ser	Gln	Ala	Val	Gly	Arg	Ser	Ser	Phe	Tyr	
			180						185					190		
tgc	ctg	gaa	tat	ttc	cct	tct	cag	atg	ctg	aga	acg	ggc	aac	aac	ttt	624
Cys	Leu	Glu	Tyr	Phe	Pro	Ser	Gln	Met	Leu	Arg	Thr	Gly	Asn	Asn	Phe	
		195					200					205				
acc	ttc	agc	tac	acc	ttt	gag	gaa	gtg	cct	ttc	cac	agc	agc	tac	gcg	672
Thr	Phe	Ser	Tyr	Thr	Phe	Glu	Glu	Val	Pro	Phe	His	Ser	Ser	Tyr	Ala	
	210					215					220					
cac	agc	cag	agc	ctg	gac	cgg	ctg	atg	aat	cct	ctc	atc	gac	caa	tac	720
His	Ser	Gln	Ser	Leu	Asp	Arg	Leu	Met	Asn	Pro	Leu	Ile	Asp	Gln	Tyr	
225					230					235					240	
ctg	tat	tac	ctg	aac	aga	act	caa	aat	cag	tcc	gga	agt	gcc	caa	aac	768
Leu	Tyr	Tyr	Leu	Asn	Arg	Thr	Gln	Asn	Gln	Ser	Gly	Ser	Ala	Gln	Asn	
				245					250					255		
aag	gac	ttg	ctg	ttt	agc	cgt	ggg	tct	cca	gct	ggc	atg	tct	gtt	cag	816
Lys	Asp	Leu	Leu	Phe	Ser	Arg	Gly	Ser	Pro	Ala	Gly	Met	Ser	Val	Gln	
			260					265					270			
ccc	aaa	aac	tgg	cta	cct	gga	ccc	tgt	tat	cgg	cag	cag	cgc	gtt	tct	864
Pro	Lys	Asn	Trp	Leu	Pro	Gly	Pro	Cys	Tyr	Arg	Gln	Gln	Arg	Val	Ser	
		275					280					285				
aaa	aca	aaa	aca	gac	aac	aac	aac	agc	aat	ttt	acc	tgg	act	ggg	gct	912
Lys	Thr	Lys	Thr	Asp	Asn	Asn	Asn	Ser	Asn	Phe	Thr	Trp	Thr	Gly	Ala	
	290					295					300					
tca	aaa	tat	aac	ctc	aat	ggg	cgt	gaa	tcc	atc	atc	aac	cct	ggc	act	960
Ser	Lys	Tyr	Asn	Leu	Asn	Gly	Arg	Glu	Ser	Ile	Ile	Asn	Pro	Gly	Thr	
305					310					315					320	
gct	atg	gcc	tca	cac	aaa	gac	gac	gaa	gac	aag	ttc	ttt	ccc	atg	agc	1008
Ala	Met	Ala	Ser	His	Lys	Asp	Asp	Glu	Asp	Lys	Phe	Phe	Pro	Met	Ser	
				325					330					335		

ggt gtc atg att ttt gga aaa gag agc gcc gga gct tca aac act gca	1056
Gly Val Met Ile Phe Gly Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala	
340 345 350	
ttg gac aat gtc atg att aca gac gaa gag gaa att aaa gcc act aac	1104
Leu Asp Asn Val Met Ile Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn	
355 360 365	
cct gtg gcc acc gaa aga ttt ggg acc gtg gca gtc aat ttc cag agc	1152
Pro Val Ala Thr Glu Arg Phe Gly Thr Val Ala Val Asn Phe Gln Ser	
370 375 380	
agc agc aca gac cct gcg acc gga gat gtg cat gct atg gga gca tta	1200
Ser Ser Thr Asp Pro Ala Thr Gly Asp Val His Ala Met Gly Ala Leu	
385 390 395 400	
cct ggc atg gtg tgg caa gat aga gac gtg tac ctg cag ggt ccc att	1248
Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile	
405 410 415	
tgg gcc aaa att cct cac aca gat gga cac ttt cac ccg tct cct ctt	1296
Trp Ala Lys Ile Pro His Thr Asp Gly His Phe His Pro Ser Pro Leu	
420 425 430	
atg ggc ggc ttt gga ctc aag aac ccg cct cct cag atc ctc atc aaa	1344
Met Gly Gly Phe Gly Leu Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys	
435 440 445	
aac acg cct gtt cct gcg aat cct ccg gcg gag ttt tca gct aca aag	1392
Asn Thr Pro Val Pro Ala Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys	
450 455 460	
ttt gct tca ttc atc acc caa tac tcc aca gga caa gtg agt gtg gaa	1440
Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu	
465 470 475 480	
att gaa tgg gag ctg cag aaa gaa aac agc aag cgc tgg aat ccc gaa	1488
Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu	
485 490 495	
gtg cag tac aca tcc aat tat gca aaa tct gcc aac gtt gat ttt act	1536
Val Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr	
500 505 510	
gtg gac aac aat gga ctt tat act gag cct cgc ccc att ggc acc cgt	1584
Val Asp Asn Asn Gly Leu Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg	
515 520 525	

tac ctt acc cgt ccc ctg taa  
 Tyr Leu Thr Arg Pro Leu  
 530

1605

<210> 17  
 <211> 534  
 <212> PRT  
 <213> AAV-1

<400> 17

Met Ala Ser Gly Gly Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala  
 1 5 10 15

Asp Gly Val Gly Asn Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp  
 20 25 30

Leu Gly Asp Arg Val Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro  
 35 40 45

Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly  
 50 55 60

Ala Ser Asn Asp Asn His Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr  
 65 70 75 80

Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln  
 85 90 95

Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe  
 100 105 110

Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val  
 115 120 125

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp  
 130 135 140

Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys  
 145 150 155 160

Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr  
 165 170 175

Leu Thr Leu Asn Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr  
 180 185 190

Cys\_Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe  
 195 200 205  
 Thr Phe Ser Tyr Thr Phe Glu Glu Val Pro Phe His Ser Ser Tyr Ala  
 210 215 220  
 His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr  
 225 230 235 240  
 Leu Tyr Tyr Leu Asn Arg Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn  
 245 250 255  
 Lys Asp Leu Leu Phe Ser Arg Gly Ser Pro Ala Gly Met Ser Val Gln  
 260 265 270  
 Pro Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser  
 275 280 285  
 Lys Thr Lys Thr Asp Asn Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala  
 290 295 300  
 Ser Lys Tyr Asn Leu Asn Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr  
 305 310 315 320  
 Ala Met Ala Ser His Lys Asp Asp Glu Asp Lys Phe Phe Pro Met Ser  
 325 330 335  
 Gly Val Met Ile Phe Gly Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala  
 340 345 350  
 Leu Asp Asn Val Met Ile Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn  
 355 360 365  
 Pro Val Ala Thr Glu Arg Phe Gly Thr Val Ala Val Asn Phe Gln Ser  
 370 375 380  
 Ser Ser Thr Asp Pro Ala Thr Gly Asp Val His Ala Met Gly Ala Leu  
 385 390 395 400  
 Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile  
 405 410 415  
 Trp Ala Lys Ile Pro His Thr Asp Gly His Phe His Pro Ser Pro Leu  
 420 425 430  
 Met Gly Gly Phe Gly Leu Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys  
 435 440 445



Asn Thr Pro Val Pro Ala Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys  
 450 455 460

Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu  
 465 470 475 480

Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu  
 485 490 495

Val Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr  
 500 505 510

Val Asp Asn Asn Gly Leu Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg  
 515 520 525

Tyr Leu Thr Arg Pro Leu  
 530

<210> 18  
 <211> 4681  
 <212> DNA  
 <213> aav-2

<400> 18  
 ttggccactc cctctctgcg cyctcgetcg ctactgagg ccgggcgacc aaaggtcgcc 60  
 cgacgccccg gctttgcccc ggcggcctca gtgagcgagc gagcgcgag agagggagtg 120  
 gccaaactcca tcactagggg ttccctggagg ggtggagtcg tgacgtgaat tacgtcatag 180  
 ggtaggggag gtcctgtatt agaggtcacg tgagtgtttt gcgacatttt gcgacaccat 240  
 gtgggtcacgc tgggtattta agcccagtg agcacgcagg gtctccattt tgaagcgggg 300  
 ggtttgaacg cgcagccgcc atgccggggt ttacgagat tgtgattaag gtccccagcg 360  
 accttgacgg gcactctgcc ggcatttctg acagctttgt gaactgggtg gccgagaagg 420  
 aatgggagtt gccgccagat tctgacatyg atctgaatct gattgagcag gcaccctga 480  
 ccgtggccga gaagctgcag cgcgactttc tgacggaatg gcgccgtgtg agtaaggccc 540  
 cggaggccct tttctttgtg caatttgaga agggagagag ctacttccac atgcacgtgc 600  
 tcgtggaaac caccggggtg aaatccatgg ttttgggacg tttcctgagt cagattcgcg 660  
 aaaaactgat tcagagaatt taccgcggga tcgagccgac tttgccaac tggttcgcg 720

tcacaaagac cagaaatggc gccggaggcg ggaacaaggt ggtggatgag tgctacatcc 780  
ccaattactt gtcceccaaa acccagcctg agctccagtg ggcgtggact aatatggaac 840  
agtatttaag cgctgtttg aatctcacgg agcgtaaacg gttggtggcg cagcatctga 900  
cgcacgtgtc gcagacgcag gagcagaaca aagagaatca gaatcccaat tctgatgcgc 960  
cggtgatcag atcaaaaact tcagccaggt acatggagct ggtcgggtgg ctcgtggaca 1020  
aggggattac ctcggagaag cagtggatcc aggaggacca ggcctcatac atctccttca 1080  
atgcggcctc caactcgcgg tcccaaatca aggtgcctt ggacaatgcg ggaaagatta 1140  
tgagcctgac taaaaccgcc ccgactacc tggtgggcca gcagcccgtg gaggacattt 1200  
ccagcaatcg gatttataaa attttggaaac taaacgggta cgatccccaat tatgcggctt 1260  
ccgtctttct gggatgggcc acgaaaaagt tcggcaagag gaacaccatc tggctgtttg 1320  
ggcctgcaac taccgggaag accaacatcg cggaggccat agcccacact gtgcccttct 1380  
acgggtgcgt aaactggacc aatgagaact ttcccttcaa cgactgtgtc gacaagatgg 1440  
tgatctggtg ggaggaggyg aagatgaccg ccaaggtcgt ggagtcggcc aaagccattc 1500  
tcggaggaag caaggtgcgc gtggaccaga aatgcaagtc ctcggcccag atagaccga 1560  
ctcccgtgat cgtcacctcc aacaccaaca tgtgcgccgt gattgacggg aactcaacga 1620  
ccttcgaaca ccagcagccg ttgcaagacc ggatgttcaa atttgaactc acccgccgtc 1680  
tggatcatga ctttgggaag gtcaccaagc aggaagtcaa agactttttc cggtgggcaa 1740  
aggatcacgt ggttgaggtg gagcatgaat tctacgtcaa aaagggtgga gccaaagaaa 1800  
gacccgcccc cagtgcgca gatataagt agcccaaacg ggtgcgcgag tcagttgcgc 1860  
agccatcgac gtcagacgcg gaagcttcga tcaactacgc agacaggtac caaaacaaat 1920  
gttctcgtca cgtgggcatg aatctgatgc tgtttccctg cagacaatgc gagagaatga 1980  
atcagaattc aaatatctgc ttcactcacg gacagaaaga ctgttttagag tgctttcccg 2040  
tgtcagaatc tcaaccggtt tctgtcgtca aaaaggcgta tcagaaactg tgctacattc 2100  
atcatatcat gggaaagggt ccagacgctt gcactgcctg cgatctggtc aatgtggatt 2160

tggatgactg catctttgaa caataaatga tttaaatcag gtatggctgc cgatggttat 2220  
cttcagatt ggctcgagga cactctctct gaaggaataa gacagtgggtg gaagctcaaa 2280  
cctggccac caccacaaa gcccgagag cggcataagg acgacagcag gggctctgtg 2340  
cttctgggt acaagtacct cggacccttc aacggactcg acaagggaga gccggtcaac 2400  
gaggcagacg ccgcggccct cgagcacgac aaagcctacg accggcagct cgacagcgga 2460  
gacaaccgt acctcaagta caaccacgcc gacgcggagt ttcaggagcg ccttaaagaa 2520  
gatacgtctt ttgggggcaa cctcggacga gcagtcttcc aggcgaaaaa gagggttctt 2580  
gaacctctcg gcctggttga ggaacctgtt aagacggctc cgggaaaaaa gaggccggtg 2640  
gagcactctc ctgtggagcc agactcctcc tcgggaaccg gaaagccggg ccagcagcct 2700  
gcaagaaaaa gattgaattt tggtcagact ggagacgcag actcagtacc tgacccccag 2760  
cctctcggac agccaccagc agccccctct ggtctgggaa ctaatacgat ggctacaggc 2820  
agtggcgcac caatggcaga caataacgag ggcgcgcagc gagtgggtaa ttcctccgga 2880  
aattggcatt gcgattccac atggatgggc gacagagtca tcaccaccag caccgaacc 2940  
tgggccctgc ccacctaaa caaccacctc tacaacaaa tttccagcca atcaggagcc 3000  
tcgaacgaca atcactactt tggctacagc accccttggg ggtattttga cttcaacaga 3060  
ttccactgcc acttttcacc acgtgactgg caaagactca tcaacaacaa ctggggattc 3120  
cgaccaaga gactcaactt caacctcttt aacattcaag tcaaagaggt cacgcagaat 3180  
gacggtacga cgacgattgc caataacctt accagcacgg ttcaggtggt tactgactcg 3240  
gagtaccagc tcccgtagct cctcggctcg gcgcatcaag gatgcctccc gccgttccca 3300  
gcagacgtct tcatggtgcc acagtatgga tacctacccc tgaacaacgg gagtcaggca 3360  
gtaggaacgt cttcatttta ctgcctggag tactttcctt ctcagatgct gcgtaccgga 3420  
aacaacttta ccttcagcta cacttttgag gacgttcctt tccacagcag ctacgctcac 3480  
agccagagtc tggaccgtct catgaatcct ctcacgacc agtacctgta ttacttgagc 3540  
agaacaaaca ctccaagtgg aaccaccagc cagtcaaggc ttcagttttc tcaggcccca 3600

gccagtgaca ttcgggacca gtctaggaac tggcttctctg gaccctgtta ccgccagcag 3660  
 cgagtatgaa agacatctgc ggataacaac aacagtgaat actcgtggac tggagctacc 3720  
 aagtaccacc tcaatggcag agactctctg gtgaatccgg ggcccggcat ggcaagccac 3780  
 aaggacgatg aagaaaagtt ttttctcag agcgggggttc tcattctttgg gaagcaaggc 3840  
 tcagagaaaa caaatgtgaa cattgaaaag gtcattgatta cagacgaaga ggaaatccca 3900  
 acaaccaatc cegtggctac ggagcagtat gggtctgtat ctaccaacct ccagagaggc 3960  
 aacagacaag cagctaccgc agatgtcaac acacaaggcg ttcttccagg catggtcttg 4020  
 caggacagag atgtgtacct tcagggggccc atctgggcaa agattccaca caggacgga 4080  
 cattttcacc cctctcccct catgggtgga ttcggactta aacaccctcc tccacagatt 4140  
 ctcatcaaga acaccccggt acctgcgaat ccttcgacca ccttcagtgc ggcaaagttt 4200  
 gcttccttca tcacacagta ctccacggga cagggtcagc gtggagatcg agtgggagct 4260  
 gcagaacgaa aacagcaaac gctggaatcc cgaaattcag tacacttcca actacaacaa 4320  
 gtctgttaat cgtggacttt accgtggata ctaatggcgt gtattcagag cctcgcccca 4380  
 ttggcaccag atacctgact cgtaatctgt aattgcttgt taatcaataa accgtttaat 4440  
 tcgtttcagt tgaactttgg tctctcgcta tttcttctt atctagtttc catggctacg 4500  
 tagataagta gcatggcggg ttaatcatta actacaagga acccctagtg atggagttgg 4560  
 ccactccctc tctgcgcgct cgctcgctca ctgaggccgg gcgaccaaag gtcgcccgcac 4620  
 gcccggtt tgccccggcg gcctcagtga gcgagcgagc gcgcagagag ggagtgggca 4680  
 a 4681

&lt;210&gt; 19

&lt;211&gt; 4683

&lt;212&gt; DNA

&lt;213&gt; aav-6

&lt;400&gt; 19

ttgycactc cctctctgcg cgctcgctcg ctactgagg ccgggcgacc aaaggtcgcc 60

cgacgcccgg gctttgcccg ggcggcctca gtgagcgagc gagcgcgag agaggggagtg 120  
gccaaactcca tcactagggg ttcttgaggg ggtggagtcg tgacgtgaat tacgtcatag 180  
ggttagggag gtcctgtatt agaggtcacg tgagtgtttt gcgacatttt gcgacaccat 240  
gtggtcacgc tgggtattta agcccagagt agcacgcagg gtctccattt tgaagcggga 300  
ggtttgaacg cgcagcgcca tgccgggggt ttacgagatt gtgattaagg tccccagcga 360  
ccttgacgag catctgcccg gcatttctga cagctttgtg aactgggtgg ccgagaagga 420  
atgggagttg ccgccagatt ctgacatgga tctgaatctg attgagcagg caccctgac 480  
cgtggccgag aagctgcagc gcgacttctt ggtccactgg cgccgcgtga gtaaggcccc 540  
ggaggccctc ttctttgttc agttcgagaa gggcgagtcc tacttccacc tccatattct 600  
ggtggagacc acgggggtca aatccatggt gctgggccgc ttctgagtc agattagcga 660  
caagctggtg cagaccatct accgcgggat cgagccgacc ctgcccaact ggttcgcggt 720  
gaccaagacg cgtaatggcg ccggaggggg gaacaagggt gtggacgagt gctacatccc 780  
caactacctc ctgcccaaga ctgagccga gctgcagtgg gcgtggacta acatggagga 840  
gtatataagc gcgtgtttaa acctggccga gcgcaaacgg ctggtggcgc acgacctgac 900  
ccacgtcagc cagaccaggt agcagaacaa ggagaatctg aacccaatt ctgacgcgcc 960  
tgtcatccgg tcaaaaacct ccgcacgcta catggagctg gtcgggtggc tgggtggaccg 1020  
gggcatcacc tccgagaagc agtggatcca ggaggaccag gcctcgtaca tctccttcaa 1080  
cgccgcctcc aactcgcggt ccagatcaa ggccgctctg gacaatgccg gcaagatcat 1140  
ggcgtgacc aaatccgcgc ccgactacct ggtaggcccc gctccgccc cgcacattaa 1200  
aaccaaccgc atttaccgca tcttgagct gaacggctac gaccctgcct acgcccggctc 1260  
cgtctttctc ggctgggccc agaaaagggt cggaaaacgc aacaccatct ggctgtttgg 1320  
gccggccacc acgggcaaga ccaacatcgc ggaagccatc gccacgccg tgcccttcta 1380  
cggtgcgtc aactggacca atgagaactt tcccttcaac gattgcgtcg acaagatggt 1440  
gatctggtgg gaggagggca agatgacggc caaggctgtg gagtccgcca aggccattct 1500

cggeggcagc aaggtgcgcg tggaccaaaa gtgcaagtcg tccgcccaga tcgatccac 1560  
ccccgtgac gtcacctcca acaccaacat gtgcgccgtg attgacggga acagcaccac 1620  
cttcgagcac cagcagccgt tgcaggaccg gatgttcaaa tttgaactca cccgccgtct 1680  
ggagcatgac tttggcaagg tgacaaagca ggaagtcaaa gagttcttcc gctgggcgca 1740  
ggatcacgtg accgaggtgg cgcattgagt ctacgtcaga aagggaggag ccaacaacag 1800  
accgcccc gatgacgcgg ataaaagcga gcccaagcgg gcctgcccct cagtcgcgga 1860  
tccatcgacg tcagacgcgg aaggagctcc ggtggacttt gccgacaggt accaaaacaa 1920  
atgttctcgt cacgcgggca tgcttcagat gctgtttccc tgcaaacat gcgagagaat 1980  
gaatcagaat ttcaacattt gcttcacgca cgggaccaga gactgttcag aatgtttccc 2040  
cggcgtgtca gaattctaac cggtcgtcag aaagaggacg tatcggaac tctgtgcat 2100  
tcatcatctg ctggggcggg ctcccagat tgcttgctcg gcctgcgac tggtaacgt 2160  
ggatctggat gactgtgtt ctgagcaata aatgacttaa accaggtatg gctgccgatg 2220  
gttatcttcc agattggctc gaggacaacc tctctgaggg cattcggcag tggtaggact 2280  
tgaaacctgg agccccgaaa cccaaagcca accagcaaaa gcaggacgac ggccggggtc 2340  
tggtagcttcc tggctacaag tacctcgac ccttcaacgg actcgacaag ggggagccc 2400  
tcaacgcggc ggatgcagc gccctcgagc acgacaaggc ctacgaccag cagctcaaag 2460  
cgggtgacaa tccgtacctg cggataacc acgccgacgc cgagtttcag gagcgtctgc 2520  
aagaagatac gtcttttggg ggcaacctcg ggcgagcagt cttccaggcc aagaagagg 2580  
ttctgaacc ttttggtctg gttgaggaag gtgctaagac ggctcctgga aagaaacgtc 2640  
cggtagagca gtcgccacaa gagccagact cctcctcggg cattggcaag acaggccagc 2700  
agcccgttaa aaagagactc aattttggtc agactggcga ctcagagtca gtccccgacc 2760  
cacaacctct cggagaacct ccagcaacct ccgtgctgt gggacctact acaatggctt 2820  
caggcgggtg cgcaccaatg gcagacaata acgaaggcgc cgacggagtg ggtaatgcct 2880  
caggaaattg gcattgcgat tccacatggc tgggcgacag agtcatcacc accagcacc 2940

gaacatgggc cttgcccacc tataacaacc acctctacaa gcaaattctcc agtgcttcaa 3000  
cgggggccag caacgacaac cactacttcg gctacagcac cccctggggg tattttgatt 3060  
tcaacagatt ccaactgccat ttctcaccac gtgactggca gcgactcatc aacaacaatt 3120  
ggggattccg gcccagaga ctcaacttca agctcttcaa catccaagtc aaggagggtca 3180  
cgacgaatga tggcgtcacg accatcgcta ataaccttac cagcacgggt caagtcttgt 3240  
cggactcgga gtaccagttc ccgtacgtcc tcggctctgc gcaccagggc tgcctccctc 3300  
cgttcccggc ggacgtgttc atgattccgc agtacggcta cctaacgctc aacaatggca 3360  
gccaggcagt gggacgctca tccttttact gcctggaata tttcccatcg cagatgctga 3420  
gaacgggcaa taactttacc ttcagctaca ccttcgagga cgtgcctttc cacagcagct 3480  
acgcgcacag ccagagcctg gaccggctga tgaatcctct catcgaccag tacctgtatt 3540  
acctgaacag aactcacaat cagtccggaa gtgccccaaa caaggacttg ctgtttagcc 3600  
gtgggtctcc agctggcatg tctgttcagc caaaaaactg gctacctgga ccctgttacc 3660  
ggcagcagcg cgttttctaaa aaaaaaacag acaacaacaa cagcaacttt acctggactg 3720  
gtgcttcaaa atataacctt aatgggctg aatctataat caaccctggc actgctatgg 3780  
cctcacacaa agacgacaaa gacaagttct tttccatgag cgggtgtcatg atttttggaa 3840  
aggagagcgc cggagcttca aacactgcat tggacaatgt catgatcaca gacgaagagg 3900  
aaatcaaagc cactaaccct gtggccaccg aaagatttgg gactgtggca gtcaatctcc 3960  
agagcagcag cacagaccct gcgaccggag atgtgcatgt tatgggagcc ttacctggaa 4020  
tggtgtggca agacagagac gtatacctgc agggctctat ttgggcaaaa attcctcaca 4080  
cggatggaca ctttcacccg tctctctca tgggaggctt tggacttaag caccgcctc 4140  
ctcagatcct catcaaaaac acgcctgttc ctgcgaatcc tccggcagag ttttcggcta 4200  
caaagtttgc ttcattcatc acccagtatt ccacaggaca agtgagcgtg gagattgaat 4260  
gggagctgca gaaagaaaac agcaaacgct ggaatcccg agtgcagtat acatctaact 4320  
atgcaaaatc tgccaacgtt gatttcactg tggacaacaa tggactttat actgagcctc 4380

gccc̄attgg caccggttac ctacccgctc cctgtaatt gtgtgttaat caataaaccg 4440  
gttaattcgt gtcagttgaa ctttggtctc atgtccttat tatcttatct ggtcaccata 4500  
gcaaccgggt acacattaac tgcttagttg cgcttcgca ataccctag tgatggagtt 4560  
gcccactccc tctatgcgcg ctgctcgtc cgggtggggcc ggcagagcag agctctgccg 4620  
tctgcggacc ttggtccgc agggcccacc gagcgagcga gcgcgcatag agggagtggc 4680  
caa 4683

<210> 20

<211> 16

<212> DNA

<213> rep binding motif

<400> 20

gctcgcgcgc tcgctg

16



## INTERNATIONAL SEARCH REPORT

Int. J. Application No

PCT/US 99/25694

## A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 -C12N15/86 C12N15/35 C12N5/10 A61K48/00

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12N A61K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	RUTLEDGE E. A. ET AL.: "Infectious clones and vectors derived from adeno-associated virus (AAV) serotypes other than AAV type 2." JOURNAL OF VIROLOGY, vol. 72, no. 1, January 1998 (1998-01), pages 309-319, XP002137089 ISSN: 0022-538X cited in the application the whole document	1-23
Y	WO 98 11244 A (SAFER BRIAN ;US HEALTH (US); CHIORINI JOHN A (US); KOTIN ROBERT M) 19 March 1998 (1998-03-19) the whole document	1-23
	-/-	

☒ Further documents are listed in the continuation of box C.☒ Patent family members are listed in annex.

## \* Special categories of cited documents:

- \*A\* document defining the general state of the art which is not considered to be of particular relevance
- \*E\* earlier document but published on or after the international filing date
- \*L\* document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- \*O\* document referring to an oral disclosure, use, exhibition or other means
- \*P\* document published prior to the international filing date but later than the priority date claimed

- \*T\* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
- \*X\* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
- \*Y\* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.
- \*&\* document member of the same patent family

Date of the actual completion of the international search

8 May 2000

Date of mailing of the international search report

22/05/2000

Name and mailing address of the ISA

European Patent Office, P.B. 5818 Patentlaan 2  
NL - 2280 HV Rijswijk  
Tel. (+31-70) 340-2040, Tx. 31 651 epo nl,  
Fax: (+31-70) 340-3016

Authorized officer

Mandl, B

# INTERNATIONAL SEARCH REPORT

Int. Patent Application No.

PCT/US 99/25694

## C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P,X	<p>XIAO W. ET AL.: "Gene therapy vectors based on adeno-associated virus type 1." JOURNAL OF VIROLOGY, vol. 73, no. 5, May 1999 (1999-05), pages 3994-4003, XP002137090  ISSN: 0022-538X  the whole document</p>	1-23

# INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 99/ 25694

## Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.:  
because they relate to subject matter not required to be searched by this Authority, namely:  
Remark: Although claims 18-20 and 22, as far as an in vivo application is concerned, are directed to a method of treatment of the human or animal body, the search has been carried out and based on the alleged effects of the compound/composition.
2. ☐ Claims Nos.:  
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:  
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

## Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

# INTERNATIONAL SEARCH REPORT

Information on patent family members

Int. l. Application No

PCT/US 99/25694

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 9811244 A	19-03-1998	AU 4645697 A EP 0932694 A	02-04-1998 04-08-1999